

FILE COPY

BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

RECEIVED

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/031772
Source: AU 1647
Date Processed by STIC: 10/18/01

89/039,177

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

RAW SEQUENCE LISTING

DATE: 10/15/2001

PATENT APPLICATION: US/09/039,177D

TIME: 13:47:03

Input Set : A:\Lud-5539 sequence listing.txt
 Output Set: N:\CRF3\10152001\I039177D.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
 5 (i) APPLICANT: Kohei MIYAZONO; Takeshi IMAMURA; Peter DEN DIJKE
 7 (ii) TITLE OF INVENTION: ISOLATED ALK-1 PROTEIN, NUCLEIC ACIDS ENCODING
 8 IT, AND USES THEREOF
 10 (iii) NUMBER OF SEQUENCES: 46
 12 (iv) CORRESPONDENCE ADDRESS:
 13 (A) ADDRESSEE: Fulbright & Jaworski L.L.P.
 14 (B) STREET: 801 Pennsylvania Avenue, N.W.
 15 (C) CITY: Washington
 16 (D) STATE: District of Columbia
 17 (E) COUNTRY: USA
 18 (F) ZIP: 20004
 20 (v) COMPUTER READABLE FORM:
 21 (A) MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
 22 (B) COMPUTER: IBM PS/2
 23 (C) OPERATING SYSTEM: PC-DOS
 24 (D) SOFTWARE: Wordperfect
 26 (vi) CURRENT APPLICATION DATA:
 27 (A) APPLICATION NUMBER: US/09/039,177D
 28 (B) FILING DATE: 13-Mar-1998
 29 (C) CLASSIFICATION: 435
 59 (vii) PRIOR APPLICATION DATA:
 32 (A) APPLICATION NUMBER: PCT/GB93/02367
 33 (B) FILING DATE: November 17, 1993
 36 (A) APPLICATION NUMBER: GB 9224057.1
 37 (B) FILING DATE: November 17, 1992
 40 (A) APPLICATION NUMBER: GB 9304677.9
 41 (B) FILING DATE: March 8, 1993
 44 (A) APPLICATION NUMBER: GB 9304680.3
 45 (B) FILING DATE: March 8, 1993
 48 (A) APPLICATION NUMBER: 9311047.6
 49 (B) FILING DATE: May 28, 1993
 52 (A) APPLICATION NUMBER: 9313763.6
 53 (B) FILING DATE: July 2, 1993
 56 (A) APPLICATION NUMBER: 9136099.2
 57 (B) FILING DATE: August 3, 1993
 60 (A) APPLICATION NUMBER: 321344.5
 61 (B) FILING DATE: October 15, 1993
 63 (viii) ATTORNEY/AGENT INFORMATION:
 64 (A) NAME: Mary Anne Schofield
 65 (B) REGISTRATION NUMBER: 36,669
 66 (C) REFERENCE/DOCKET NUMBER: LUD 5539 CIP - JEL/MAS
 68 (ix) TELECOMMUNICATION INFORMATION:
 69 (A) TELEPHONE: (202) 662-0200
 70 (B) TELEFAX: (202) 662-4643

Does Not Comply
 Corrected Diskette Needed

See page 2, 4, 5, 6
 and 7

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001
TIME: 13:47:03

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRF3\10152001\I039177D.raw

ERRORED SEQUENCES

74 (2) INFORMATION FOR SEQ ID NO: 1:
75 (i) SEQUENCE CHARACTERISTICS:
76 (A) LENGTH: 1984 base pairs
77 (B) TYPE: nucleic acid
78 (C) STRANDEDNESS: unknown
79 (D) TOPOLOGY: linear
81 (ii) MOLECULE TYPE: cDNA
83 (iii) HYPOTHETICAL: NO
C--> 85 (iv) ANTI-SENSE: NO
87 (v) FRAGMENT TYPE: internal
89 (vi) ORIGINAL SOURCE:
90 (A) ORGANISM: Homo sapiens
92 (ix) FEATURE:
93 (A) NAME/KEY: CDS
94 (B) LOCATION: 283..1791
96 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

E--> 98 AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGGCCA GGCAGGAAGA
99 CGCTGGAATA 60

E--> 101 AGAAACATTT TTGCTCCAGC CCCCATCCCA GTCCCGGGAG GCTGCCGCC
102 CAGCTGCGCC 120

E--> 104 GAGCGAGGCC CTCCCCGGCT CCAGCCCGGT CGGGGGCCGC GCCGGACCCC
105 AGCCCGCCGT 180

E--> 107 CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC
108 GGTCCGCCGA 240

E--> 110 AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CC ATG ACC TTG GGC

W--> 111 294

Does Not Comply
Corrected Diskette Needed

Met Thr Leu Gly

1

112
113
114 TCC CCC AGG AAA GGC CTT CTG ATG CTG CTG ATG GCC TTG GTG ACC CAG 342
115 Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala Leu Val Thr Gln
116 5 10 15 20
118 GGA GAC CCT GTG AAG CCG TCT CGG GGC CCG CTG GTG ACC TGC ACG TGT 390
119 Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val Thr Cys Thr Cys
120 25 30 35
122 GAG AGC CCA CAT TGC AAG GGG CCT ACC TGC CGG GGG GCC TGG TGC ACA 438
123 Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly Ala Trp Cys Thr
124 40 45 50
126 GTA GTG CTG GTG CGG GAG GGG AGG CAC CCC CAG GAA CAT CGG GGC 486
127 Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln Glu His Arg Gly
128 ' 55 60 65
130 TGC GGG AAC TTG CAC AGG GAG CTC TGC AGG GGG CGC CCC ACC GAG TTC 534
131 Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg Pro Thr Glu Phe
132 70 75 80
134 GTC AAC CAC TAC TGC GAC AGC CAC CTC TGC AAC CAC AAC GTG TCC 582
135 Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn His Asn Val Ser
136 85 90 95 100
138 CTG GTG CTG GAG GCC ACC CAA CCT CCT TCG GAG CAG CCG GGA ACA GAT 630
139 Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln Pro Gly Thr Asp

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001

TIME: 13:47:03

Input Set : A:\Lud-5539 sequence listing.txt
 Output Set: N:\CRF3\10152001\I039177D.raw

140	105	110	115	
142	GGC CAG CTG GCC CTG ATC CTG GGC CCC GTG CTG GCC TTG CTG GCC CTG			678
143	Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala Leu Leu Ala Leu			
144	120	125	130	
146	GTG GCC CTG GGT GTC CTG GGC CTG TGG CAT GTC CGA CGG AGG CAG GAG			726
147	Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg Arg Arg Gln Glu			
148	135	140	145	
150	AAG CAG CGT GGC CTG CAC AGC GAG CTG GGA GAG TCC AGT CTC ATC CTG			774
151	Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser Ser Leu Ile Leu			
152	150	155	160	
154	AAA GCA TCT GAG CAG GGC GAC ACG ATG TTG GGG GAC CTC CTG GAC AGT			822
155	Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp Leu Leu Asp Ser			
156	165	170	175	180
158	GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG			870
159	Asp Cys Thr Thr Gly Ser Gly Leu Pro Phe Leu Val Gln Arg			
160	185	190	195	
162	ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC			918
163	Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly Lys Gly Arg			
164	200	205	210	
166	TAT GGC GAA GTG TGG CGG GGC TTG TGG CAC GGT GAG AGT GTG GCC GTC			966
167	Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu Ser Val Ala Val			
168	215	220	225	
170	AAG ATC TTC TCC TCG AGG GAT GAA CAG TCC TGG TTC CGG GAG ACT GAG			1014
171	Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg Glu Thr Glu			
172	230	235	240	
174	ATC TAT AAC ACA GTA TTG CTC AGA CAC GAC AAC ATC CTA GGC TTC ATC			1062
175	Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu Gly Phe Ile			
176	245	250	255	260
178	GCC TCA GAC ATG ACC TCC CGC AAC TCG ACG CAG CTG TGG CTC ATC			1110
179	Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu Trp Leu Ile			
180	265	270	275	
182	ACG CAC TAC CAC GAG CAC GGC TCC CTC TAC GAC TTT CTG CAG AGA CAG			1158
183	Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu Gln Arg Gln			
184	280	285	290	
186	ACG CTG GAG CCC CAT CTG GCT CTG AGG CTA GCT GTG TCC GCG GCA TGC			1206
187	Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val Ser Ala Ala Cys			
188	295	300	305	
190	GGC CTG GCG CAC CTG CAC GTG GAG ATC TTC GGT ACA CAG GGC AAA CCA			1254
191	Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln Gly Lys Pro			
192	310	315	320	
194	GCC ATT CCC CAC CGC GAC TTC AAG AGC CGC AAT GTG CTG GTC AAG AGC			1302
195	Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val Leu Val Lys Ser			
196	325	330	335	340
198	AAC CTG CAG TGT TGC ATC GCC GAC CTG GGC CTG GCT GTG ATG CAC TCA			1350
199	Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Met His Ser			
200	345	350	355	
202	CAG GGC AGC GAT TAC CTG GAC ATC GGC AAC AAC CCG AGA GTG GGC ACC			1398
203	Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro Arg Val Gly Thr			
204	360	365	370	

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001
TIME: 13:47:03

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRF3\10152001\I039177D.raw

E--> 206 AAG CGG TAC ATG GCA CCC GAG GTG CTG GAC GAG CAG ATC CGC ACG GAC
 W--> 207 1446 *measured end number*
 208 Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln Ile Arg Thr Asp
 W--> 209 375 380 385
 211 TGC TTT GAG TCC TAC AAG TGG ACT GAC ATC TGG GCC TTT GGC CTG GTG 1494
 212 Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe Gly Leu Val
 W--> 213 390 395 400
 215 CTG TGG GAG ATT GCC CGC CGG ACC ATC GTG AAT GGC ATC GTG GAG GAC 1542
 216 Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly Ile Val Glu Asp
 W--> 217 405 410 415 420
 219 TAT AGA CCA CCC TTC TAT GAT GTG GTG CCC AAT GAC CCC AGC TTT GAG 1590
 220 Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp Pro Ser Phe Glu
 W--> 221 425 430 435
 223 GAC ATG AAG AAG GTG GTG TGT GTG GAT CAG CAG ACC CCC ACC ATC CCT 1638
 224 Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr Ile Pro
 W--> 225 440 445 450
 227 AAC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA GCT CAG ATG ATG 1686
 228 Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln Met Met
 W--> 229 455 460 465
 231 CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC ACC GCG CTG CGG 1734
 232 Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg
 W--> 233 470 475 480
 E--> 235 ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA GAG AAG CCT AAA
 W--> 236 1782
 237 Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys Pro Lys
 W--> 238 485 490 495 500
 240 GTG ATT CAA TAGCCCAGGA GCACCTGATT CCTTTCTGCC TGCAGGGGGC 1831
 241 Val Ile Gln
 E--> 243 TGGGGGGGTG GGGGGCAGTG GATGGTGCCT TATCTGGTA GAGGTAGTGT
 244 GAGTGTGGTG 1891
 E--> 246 TGTGCTGGGG ATGGGCAGCT GCGCCTGCCT GCTCGGCCCC CAGCCCACCC
 247 AGCCAAAAT 1951
 249 ACAGCTGGGC TGAAACCTGA AAAAAAAA AAA 1984
 329 (2) INFORMATION FOR SEQ ID NO: 3:
 330 (i) SEQUENCE CHARACTERISTICS:
 331 (A) LENGTH: 2724 base pairs
 332 (B) TYPE: nucleic acid
 333 (C) STRANDEDNESS: unknown
 334 (D) TOPOLOGY: linear
 336 (ii) MOLECULE TYPE: cDNA
 338 (iii) HYPOTHETICAL: NO
 C--> 340 (iv) ANTI-SENSE: NO *should include this field*
 342 (v) FRAGMENT TYPE: internal
 344 (vi) ORIGINAL SOURCE:
 345 (A) ORGANISM: Homo sapiens
 347 (ix) FEATURE:
 348 (A) NAME/KEY: CDS
 349 (B) LOCATION: 104..1630
 351 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001
TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRF3\10152001\I039177D.raw

E--> 353 ~~CTCCGAGTAC CCCAGTGACC AGAGTGAGAG AAGCTCTGAA CGAGGGCACG~~ *Wronged Nucleotides*
 E--> 354 ~~CGGCTTGAAAG~~ 60
 E--> 356 ~~GACTGTGGCC AGATGTGACC AAGAGCCTGC ATTAAGTTGT ACA ATG GTA GAT GGA~~
 W--> 357 115
 358 Met Val Asp Gly
 359 1
 361 GTG ATG ATT CTT CCT GTG CTT ATC ATG ATT GCT CTC CCC TCC CCT AGT 163
 362 Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu Pro Ser Pro Ser
 363 5 10 15 20
 365 ATG GAA GAT GAG AAG CCC AAG GTC AAC CCC AAA CTC TAC ATG TGT GTG 211
 366 Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu Tyr Met Cys Val
 367 25 30 35
 369 TGT GAA GGT CTC TCC TGC GGT AAT GAG GAC CAC TGT GAA GGC CAG CAG 259
 370 Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys Glu Gly Gln Gln
 371 40 45 50
 373 TGC TTT TCC TCA CTG AGC ATC AAC GAT GGC TTC CAC GTC TAC CAG AAA 307
 374 Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His Val Tyr Gln Lys
 375 55 60 65
 377 GGC TGC TTC CAG GTT TAT GAG CAG GGA AAG ATG ACC TGT AAG ACC CCG 355
 378 Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr Cys Lys Thr Pro
 379 70 75 80
 381 CCG TCC CCT GGC CAA GCT GTG GAG TGC TGC CAA GGG GAC TGG TGT AAC 403
 382 Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly Asp Trp Cys Asn
 383 85 90 95 100
 385 AGG AAC ATC ACG GCC CAG CTG CCC ACT AAA GGA AAA TCC TTC CCT GGA 451
 386 Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys Ser Phe Pro Gly
 387 105 110 115
 389 ACA CAG AAT TTC CAC TTG GAG GTT GGC CTC ATT ATT CTC TCT GTA GTG 499
 390 Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile Leu Ser Val Val
 391 120 125 130
 393 TTC GCA GTA TGT CTT TTA GCC TGC CTG CTG GGA GTT GCT CTC CGA AAA 547
 394 Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val Ala Leu Arg Lys
 395 135 140 145
 397 TTT AAA AGG CGC AAC CAA GAA CGC CTC AAT CCC CGA GAC GTG GAG TAT 595
 398 Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg Asp Val Glu Tyr
 399 150 155 160
 401 GGC ACT ATC GAA GGG CTC ATC ACC ACC AAT GTT GGA GAC AGC ACT TTA 643
 402 Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly Asp Ser Thr Leu
 403 165 170 175 180
 405 GCA GAT TTA TTG GAT CAT TCG TGT ACA TCA GGA AGT GGC TCT GGT CTT 691
 406 Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser Gly Leu
 407 185 190 195
 409 CCT TTT CTG GTA CAA AGA ACA GTG GCT CGC CAG ATT ACA CTG TTG GAG 739
 410 Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile Thr Leu Leu Glu
 411 200 205 210
 413 TGT GTC GGG AAA GGC AGG TAT GGT GAG GTG TGG AGG GGC AGC TGG CAA 787
 414 Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp Gln
 415 215 220 225
 417 GGG GAA AAT GTT GCC GTG AAG ATC TTC TCC TCC CGT GAT GAG AAG TCA 835

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001
TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRF3\10152001\I039177D.raw

418	Gly	Glu	Asn	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Lys	Ser			
419	230				235				240										
421	TGG	TTC	AGG	GAA	ACG	GAA	TTG	TAC	AAC	ACT	GTG	ATG	CTG	AGG	CAT	GAA	883		
422	Trp	Phe	Arg	Glu	Thr	Glu	Leu	Tyr	Asn	Thr	Val	Met	Leu	Arg	His	Glu			
423	245.				250				255			260							
425	AAT	ATC	TTA	GGT	TTC	ATT	GCT	TCA	GAC	ATG	ACA	TCA	AGA	CAC	TCC	AGT	931		
426	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser	Arg	His	Ser	Ser			
427					265				270			275							
429	ACC	CAG	CTG	TGG	TTA	ATT	ACA	CAT	TAT	CAT	GAA	ATG	GGA	TCG	TTG	TAC	979		
430	Thr	Gln	Leu	Trp	Leu	Ile	Thr	His	Tyr	His	Glu	Met	Gly	Ser	Leu	Tyr			
431					280				285			290							
433	GAC	TAT	CTT	CAG	CTT	ACT	ACT	CTG	GAT	ACA	GTT	AGC	TGC	CTT	CGA	ATA	1027		
434	Asp	Tyr	Leu	Gln	Leu	Thr	Thr	Leu	Asp	Thr	Val	Ser	Cys	Leu	Arg	Ile			
435					295				300			305							
437	GTT	CTG	TCC	ATA	GCT	AGT	GGT	CTT	GCA	CAT	TTG	CAC	ATA	GAG	ATA	TTT	1075		
438	Val	Leu	Ser	Ile	Ala	Ser	Gly	Leu	Ala	His	Leu	His	Ile	Glu	Ile	Phe			
439					310				315			320							
E-->	441	GGG	ACC	CAA	GGG	AAA	CCA	GCC	ATT	GCC	CAT	CGA	GAT	TTA	AAG	AGC	AAA		
W-->	442	1123																	
	443	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Lys		
W-->	444	325					330			335			340						
	446	AAT	ATT	CTG	GTG	TTT	AAG	AAG	AAT	GGA	CAG	TGT	TGC	ATA	GCA	GAT	TTG	GGC	1171
	447	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Gln	Cys	Cys	Ile	Ala	Asp	Leu	Gly		
W-->	448						345			350			355						
	450	CTG	GCA	GTC	ATG	CAT	TCC	CAG	AGC	ACC	AAT	CAG	CTT	GAT	GTG	GGG	AAC		
	451	Leu	Ala	Val	Met	His	Ser	Gln	Ser	Thr	Asn	Gln	Leu	Asp	Val	Gly	Asn		
W-->	452						360			365			370						
	454	AAT	CCC	CGT	GTG	GGC	ACC	AAG	CGC	TAC	ATG	GCC	CCC	GAA	GTT	CTA	GAT	1267	
	455	Asn	Pro	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp		
W-->	456						375			380			385						
	458	GAA	ACC	ATC	CAG	GTG	GAT	TGT	TTC	GAT	TCT	TAT	AAA	AGG	GTC	GAT	ATT	1315	
	459	Glu	Thr	Ile	Gln	Val	Asp	Cys	Phe	Asp	Ser	Tyr	Lys	Arg	Val	Asp	Ile		
W-->	460						390			395			400						
	462	TGG	GCC	TTT	GGA	CTT	GTG	TTG	TGG	GAA	GTG	GCC	AGG	CGG	ATG	GTG	AGC	1363	
	463	Trp	Ala	Phe	Gly	Leu	Val	Leu	Trp	Glu	Val	Ala	Arg	Arg	Met	Val	Ser		
W-->	464	405					410			415			420						
	466	AAT	GGT	ATA	GTG	GAG	GAT	TAC	AAG	CCA	CCG	TTC	TAC	GAT	GTG	GTT	CCC	1411	
	467	Asn	Gly	Ile	Val	Glu	Asp	Tyr	Lys	Pro	Pro	Phe	Tyr	Asp	Val	Val	Pro		
W-->	468						425			430			435						
	470	AAT	GAC	CCA	AGT	TTT	GAA	GAT	ATG	AGG	AAG	GTA	GTC	TGT	GTG	GAT	CAA	1459	
	471	Asn	Asp	Pro	Ser	Phe	Glu	Asp	Met	Arg	Lys	Val	Val	Cys	Val	Asp	Gln		
W-->	472						440			445			450						
	474	CAA	AGG	CCA	AAC	ATA	CCC	AAC	AGA	TGG	TTC	TCA	GAC	CCG	ACA	TTA	ACC	1507	
	475	Gln	Arg	Pro	Asn	Ile	Pro	Asn	Arg	Trp	Phe	Ser	Asp	Pro	Thr	Leu	Thr		
W-->	476						455			460			465						
	478	TCT	CTG	GCC	AAG	CTA	ATG	AAA	GAA	TGC	TGG	TAT	CAA	AAT	CCA	TCC	GCA	1555	
	479	Ser	Leu	Ala	Lys	Leu	Met	Lys	Glu	Cys	Trp	Tyr	Gln	Asn	Pro	Ser	Ala		
W-->	480						470			475			480						
	482	AGA	CTC	ACA	GCA	CTG	CGT	ATC	AAA	AAG	ACT	TTG	ACC	AAA	ATT	GAT	AAT	1603	

not aligned
end of string
new numbering
not aligned
new numbering

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001
TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRF3\10152001\I039177D.raw

483 Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr Lys Ile Asp Asn
W--> 484 485 490 495 500 1650
486 TCC CTC GAC AAA TTG AAA ACT GAC TGT TGACATTTTC ATAGTGTCAA
487 Ser Leu Asp Lys Leu Lys Thr Asp Cys
W--> 488 505
E--> 490 ~~GAAGGAAGAT TTGACGTTGT~~ TGTCATTGTC CAGCTGGAC CTAATGCTGG *Unapped nucleotides*
491 CCTGACTGGT 1710
E--> 493 ~~TGTCAGAATG GAATCAGTCT~~ GTCTCCCTCC CCAAATGGCT GCTTGACAA
494 GGCAGACGTC 1770
E--> 496 GTACCCAGCC ATGTGTTGGG GAGACATCAA AACCACCCCTA ACCTCGCTCG
497 ATGACTGTGA 1830
E--> 499 ACTGGGCATT TCACGAAC TG TTCACACTGC AGAGACTAAT GTTGGACAGA
500 CACTGTTGCA 1890
E--> 502 AAGGTAGGGA CTGGAGGAAC ACAGAGAAAT CCTAAAAGAG ATCTGGGCAT
503 TAAGTCAGTG 1950
E--> 505 GCTTGCATA GCTTCACAA GTCTCCTAGA CACTCCCCAC GGGAAACTCA
506 AGGAGGTGGT 2010
E--> 508 GAATTTTAA TCAGCAATAT TGCCTGTGCT TCTCTTCTTT ATTGCCTAG
509 GAATTCTTTG 2070
E--> 511 CATTCCCTTAC TTGCACTGTT ACTCTTAATT TTAAAGACCC AACTTGCCAA
512 AATGTTGGCT 2130
E--> 514 GCGTACTCCA CTGGTCTGTC TTTGGATAAT AGGAATTCAA TTTGGAAAAA
515 CAAAATGTA 2190
E--> 517 TGTCAGACTT TGCTGCATT TACACATGTG CTGATGTTA CAATGATGCC
518 GAACATTAGG 2250
E--> 520 AATTGTTTAT ACACAACCTT GCAAATTATT TATTACTTGT GCACTTAGTA
521 GTTTTACAA 2310
E--> 523 AACTGCTTTG TGCAATATGTT AAAGCTTATT TTTATGTGGT CTTATGATTT
524 TATTACAGAA 2370
E--> 526 ATGTTTTAA CACTATACTC TAAAATGGAC ATTTCTTTT ATTATCAGTT
527 AAAATCACAT 2430
E--> 529 TTTAAGTGCT TCACATTGTT ATGTGTGTAG ACTGTAACCT TTTTCAGTT
530 CATATGCAGA 2490
E--> 532 ACGTATTTAG CCATTACCCA CGTGACACCA CCGAATATAT TATCGATTTA
533 GAAGCAAAGA 2550
E--> 535 TTTCAGTAGA ATTTTAGTCC TGAACGCTAC GGGGAAAATG CATTTCCTTC
536 AGAATTATCC 2610
E--> 538 ATTACGTGCA TTTAAACTCT GCCAGAAAAA AATAACTATT TTGTTTAAT
539 CTACTTTTG 2670
E--> 541 TATTTAGTAG TTATTGTAT AAATTAAATA AACTGTTTC AAGTCAAAAA AAAA
W--> 542 2724
621 (2) INFORMATION FOR SEQ ID NO: 5:
622 (i) SEQUENCE CHARACTERISTICS:
623 (A) LENGTH: 2932 base pairs
624 (B) TYPE: nucleic acid
625 (C) STRANDEDNESS: unknown
626 (D) TOPOLOGY: linear
628 (ii) MOLECULE TYPE: cDNA
630 (iii) HYPOTHETICAL: NO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001
TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRF3\10152001\I039177D.raw

C--> 632 (iv) ANTI-SENSE: NO
634 (v) FRAGMENT TYPE: internal
636 (vi) ORIGINAL SOURCE:
637 (A) ORGANISM: Homo sapiens
639 (ix) FEATURE:
640 (A) NAME/KEY: CDS
641 (B) LOCATION: 310..1905
643 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
E--> 645 GCTCCGCGCC GAGGGCTGGA GGATGCGTTC CCTGGGGTCC GGACTTATGA
646 AAATATGCAT 60
E--> 648 CAGTTAATA CTGTCTTGGGA ATTCATGAGA TGGAAGCATA GGTCAAAGCT
649 GTTGGAGAA 120
E--> 651 AATCAGAAGT ACAGTTTAT CTAGCCACAT CTTGGAGGAG TCGTAAGAAA
652 GCAGTGGGAG 180
E--> 654 TTGAAGTCAT TGTCAAGTGC TTGCGATCTT TTACAAGAAA ATCTCACTGA
655 ATGATAGTCA 240
E--> 657 TTAAATTGG TGAAGTAGCA AGACCAATTAA TTAAAGGTGA CAGTACACAG
658 GAAACATTAC 300
660 AATTGAACA ATG ACT CAG CTA TAC ATT TAC ATC AGA TTA TTG GGA GCC 348
661 Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala
662 1 5 10
664 TAT TTG TTC ATC ATT TCT CGT GTT CAA GGA CAG AAT CTG GAT AGT ATG 396
665 Tyr Leu Phe Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met
666 15 20 25
668 CTT CAT GGC ACT GGG ATG AAA TCA GAC TCC GAC CAG AAA AAG TCA GAA 444
669 Leu His Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu
670 30 35 40 45
672 AAT GGA GTA ACC TTA GCA CCA GAG GAT ACC TTG CCT TTT TTA AAG TGC 492
673 Asn Gly Val Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys
674 50 55 60
676 TAT TGC TCA GGG CAC TGT CCA GAT GAT GCT ATT AAT AAC ACA TGC ATA 540
677 Tyr Cys Ser Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile
678 65 70 75
680 ACT AAT GGA CAT TGC TTT GCC ATC ATA GAA GAA GAT GAC CAG GGA GAA 588
681 Thr Asn Gly His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu
682 80 85 90
684 ACC ACA TTA GCT TCA GGG TGT ATG AAA TAT GAA GGA TCT GAT TTT CAG 636
685 Thr Thr Leu Ala Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln
686 95 100 105
688 TGC AAA GAT TCT CCA AAA GCC CAG CTA CGC CGG ACA ATA GAA TGT TGT 684
689 Cys Lys Asp Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys
690 110 115 120 125
692 CGG ACC AAT TTA TGT AAC CAG TAT TTG CAA CCC ACA CTG CCC CCT GTT 732
693 Arg Thr Asn Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val
694 130 135 140
696 GTC ATA GGT CCG TTT TTT GAT GGC AGC ATT CGA TGG CTG GTT TTG CTC 780
697 Val Ile Gly Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Leu Leu
698 145 150 155
700 ATT TCT ATG GCT GTC TGC ATA ATT GCT ATG ATC ATC TTC TCC AGC TGC 828

RAW SEQUENCE LISTING DATE: 10/15/2001
 PATENT APPLICATION: US/09/039,177D. TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
 Output Set: N:\CRF3\10152001\I039177D.raw

701	Ile Ser Met Ala Val Cys Ile Ile Ala Met Ile Ile Phe Ser Ser Cys			
702	160	165	170	
704	TTT TGT TAC AAA CAT TAT TGC AAG AGC ATC TCA AGC AGA CGT CGT TAC		876	
705	Phe Cys Tyr Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Arg Arg Tyr			
706	175	180	185	
708	AAT CGT GAT TTG GAA CAG GAT GAA GCA TTT ATT CCA GTT GGA GAA TCA		924	
709	Asn Arg Asp Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser			
710	190	195	200	205
712	CTA AAA GAC CTT ATT GAC CAG TCA CAA AGT TCT GGT AGT GGG TCT GGA		972	
713	Leu Lys Asp Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly			
714	210	215	220	
716	CTA CCT TTA TTG GTT CAG CGA ACT ATT GCC AAA CAG ATT CAG ATG GTC		1020	
717	Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val			
718	225	230	235	
E-->	720 CGG CAA GTT GGT AAA GGC CGA TAT GGA GAA GTA TGG ATG GGC AAA TGG			
W-->	721 1068			
	722 Arg Gln Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp			
W-->	723 240	245	250	
	725 CGT GGC GAA AAA GTG GCG GTG AAA GTA TTC TTT ACC ACT GAA GAA GCC		1116	
	726 Arg Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala			
W-->	727 255	260	265	
	729 AGC TGG TTT CGA GAA ACA GAA ATC TAC CAA ACT GTG CTA ATG CGC CAT		1164	
	730 Ser Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His			
W-->	731 270	275	280	285
	733 GAA AAC ATA CTT GGT TTC ATA GCG GCA GAC ATT AAA GGT ACA GGT TCC		1212	
	734 Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser			
W-->	735 290	295	300	
	737 TGG ACT CAG CTC TAT TTG ATT ACT GAT TAC CAT GAA AAT GGA TCT CTC		1260	
	738 Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu			
W-->	739 305	310	315	
	741 TAT GAC TTC CTG AAA TGT GCT ACA CTG GAC ACC AGA GCC CTG CTT AAA		1308	
	742 Tyr Asp Phe Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys			
W-->	743 320	325	330	
	745 TTG GCT TAT TCA GCT GCC TGT GGT CTG TGC CAC CTG CAC ACA GAA ATT		1356	
	746 Leu Ala Tyr Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile			
W-->	747 335	340	345	
	749 TAT GGC ACC CAA GGA AAG CCC GCA ATT GCT CAT CGA GAC CTA AAG AGC		1404	
	750 Tyr Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser			
W-->	751 350	355	360	365
	753 AAA AAC ATC CTC ATC AAG AAA AAT GGG AGT TGC TGC ATT GCT GAC CTG		1452	
	754 Lys Asn Ile Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu			
W-->	755 370	375	380	
	757 GGC CTT GCT GTT AAA TTC AAC AGT GAC ACA AAT GAA GTT GAT GTG CCC		1500	
	758 Gly Leu Ala Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Val Pro			
W-->	759 385	390	395	
	761 TTG AAT ACC AGG GTG GGC ACC AAA CGC TAC ATG GCT CCC GAA GTG CTG		1548	
	762 Leu Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu			
W-->	763 400	405	410	
	765 GAC GAA AGC CTG AAC AAA AAC CAC TTC CAG CCC TAC ATC ATG GCT GAC		1596	

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001

TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
 Output Set: N:\CRF3\10152001\I039177D.raw

766	Asp	Glu	Ser	Leu	Asn	Lys	Asn	His	Phe	Gln	Pro	Tyr	Ile	Met	Ala	Asp	
W--> 767	415				420								425				
769	ATC	TAC	AGC	TTC	GGC	CTA	ATC	ATT	TGG	GAG	ATG	GCT	CGT	CGT	TGT	ATC	1644
770	Ile	Tyr	Ser	Phe	Gly	Leu	Ile	Ile	Trp	Glu	Met	Ala	Arg	Arg	Cys	Ile	
W--> 771	430				435					440				445			
773	ACA	GGA	GGG	ATC	GTG	GAA	GAA	TAC	CAA	TTG	CCA	TAT	TAC	AAC	ATG	GTA	1692
774	Thr	Gly	Gly	Ile	Val	Glu	Glu	Tyr	Gln	Leu	Pro	Tyr	Tyr	Asn	Met	Val	
W--> 775					450					455				460			
777	CCG	AGT	GAT	CCG	TCA	TAC	GAA	GAT	ATG	CGT	GAG	GTT	GTG	TGT	GTC	AAA	1740
778	Pro	Ser	Asp	Pro	Ser	Tyr	Glu	Asp	Met	Arg	Glu	Val	Val	Cys	Val	Lys	
W--> 779					465					470				475			
781	CGT	TTG	CGG	CCA	ATT	GTG	TCT	AAT	CGG	TGG	AAC	AGT	GAT	GAA	TGT	CTA	1788
782	Arg	Leu	Arg	Pro	Ile	Val	Ser	Asn	Arg	Trp	Asn	Ser	Asp	Glu	Cys	Leu	
W--> 783					480					485				490			
785	CGA	GCA	GTT	TTG	AAG	CTA	ATG	TCA	GAA	TGC	TGG	GCC	CAC	AAT	CCA	GCC	1836
786	Arg	Ala	Val	Leu	Lys	Leu	Met	Ser	Glu	Cys	Trp	Ala	His	Asn	Pro	Ala	
W--> 787					495					500				505			
789	TCC	AGA	CTC	ACA	GCA	TTG	AGA	ATT	AAG	AAG	ACG	CTT	GCC	AAG	ATG	GTT	1884
790	Ser	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Ala	Lys	Met	Val	
W--> 791					510					515				520		525	
E--> 793	GAA	TCC	CAA	GAT	GTA	AAA	ATC	TGATGGTTAA	ACCATCGGAG	GAGAAACTCT							
W--> 794		1935															
	795	Glu	Ser	Gln	Asp	Val	Lys	Ile									
W--> 796					530												
E--> 798	AGACTGCAAG	AACTGTTTT	ACCCATGGCA	TGGGTGGAAT	TAGAGTGGAA												
799	TAAGGATGTT		1995														
E--> 801	AACTGGTTC	TCAGACTCTT	TCTTCACTAC	GTGTTCACAG	GCTGCTAATA												
802	TTAACACTTT		2055														
E--> 804	CAGTACTCTT	ATTAGGATAC	AAGCTGGAA	CTTCTAAACA	CTTCATTCTT												
805	TATATATGGA		2115														
E--> 807	CAGCTTTATT	TTAAATGTGG	TTTTGATGC	CTTTTTTAA	GTGGGTTTT												
808	ATGAACTGCA		2175														
E--> 810	TCAAGACTTC	AATCCTGATT	AGTGTCTCCA	GTCAAGCTCT	GGGTACTGAA												
811	TTGCCTGTT		2235														
E--> 813	ATAAAACGGT	GCTTTCTGTG	AAAGCCTAA	GAAGATAAAT	GAGCGCAGCA												
814	GAGATGGAGA		2295														
E--> 816	AATAGACTTT	GCCTTTACC	TGAGACATTC	AGTCGTTTG	TATTCTACCT												
817	TTGTAAAACA		2355														
E--> 819	GCCTATAGAT	GATGATGTGT	TTGGGATACT	GCTTATTTTA	TGATAGTTG												
820	TCCGTGTC		2415														
E--> 822	TTAGTGTGATG	GTGTGTGTC	CCATGCACAT	GCACGCCGGG	ATTCCCTCTGC												
823	TGCCATTGTA		2475														
E--> 825	ATTAGAAGAA	AATAATTAT	ATGCATGCAC	AGGAAGATAT	TGGTGGCCGG												
826	TGGTTTGTG		2535														
E--> 828	CTTAAAAAAT	GCAATATCTG	ACCAAGATTC	GCCAATCTCA	TACAAGCCAT												
829	TTACTTTGCA		2595														
E--> 831	AGTGAGATAG	CTTCCCCACC	AGCTTTATTT	TTAACATGA	AAGCTGATGC												
832	CAAGGCCAAA		2655														
E--> 834	AGAAGTTAA	AGCATCTGTA	AATTTGGACT	GTTCCTTC	AACCACCATT												

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001
TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRF3\10152001\I039177D.raw

835	TTTTTGTGG	2715				
E--> 837	TTATTATTT	TGTCACGGAA	AGCATCCTCT	CCAAAGTTGG	AGCTTCTATT	
838	GCCATGAACC	2775				
E--> 840	ATGCTTACAA	AGAAAGCACT	TCTTATTGAA	GTGAATTCT	GCATTTGATA	
841	GCAATGTAAG	2835				
E--> 843	TGCCCTATAAC	CATGTTCTAT	ATTCTTTATT	CTCAGTAACT	TTTAAAAGGG	
844	AAGTTATTAA	2895				
846	TATTTGTGT	ATAATGTGCT	TTATTTGCAA	ATCACCC	2932	
929	(2) INFORMATION FOR SEQ ID NO: 7:					
930	(i) SEQUENCE CHARACTERISTICS:					
931	(A) LENGTH: 2333 base pairs					
932	(B) TYPE: nucleic acid					
933	(C) STRANDEDNESS: unknown					
934	(D) TOPOLOGY: linear					
936	(ii) MOLECULE TYPE: cDNA					
938	(iii) HYPOTHETICAL: NO					
C--> 940	(iv) ANTI-SENSE: NO					
942	(v) FRAGMENT TYPE: internal					
944	(vi) ORIGINAL SOURCE:					
945	(A) ORGANISM: Homo sapiens					
947	(ix) FEATURE:					
948	(A) NAME/KEY: CDS					
949	(B) LOCATION: 1..1515					
951	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:					
953	ATG GCG GAG TCG GCC GGA GCC TCC TCC TTC CCC CTT GTT GTC CTC	48				
954	Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu					
955	1 5 10 15					
957	CTG CTC GCC GGC AGC GGC GGG TCC GGG CCC CGG GGG GTC CAG GCT CTG	96				
958	Leu Leu Ala Gly Ser Gly Ser Gly Pro Arg Gly Val Gln Ala Leu					
959	20 25 30					
961	CTG TGT GCG TGC ACC AGC TGC CTC CAG GCC AAC TAC ACG TGT GAG ACA	144				
962	Leu Cys Ala Cys Thr Ser Cys Leu Gln Ala Asn Tyr Thr Cys Glu Thr					
963	35 40 45					
965	GAT GGG GCC TGC ATG GTT TCC TTT TTC AAT CTG GAT GGG ATG GAG CAC	192				
966	Asp Gly Ala Cys Met Val Ser Phe Phe Asn Leu Asp Gly Met Glu His					
967	50 55 60					
969	CAT GTG CGC ACC TGC ATC CCC AAA GTG GAG CTG GTC CCT GCC GGG AAG	240				
970	His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys					
971	65 70 75 80					
973	CCC TTC TAC TGC CTG AGC TCG GAG GAC CTG CGC AAC ACC CAC TGC TGC	288				
974	Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys					
975	85 90 95					
977	TAC ACT GAC TAC TGC AAC AGG ATC GAC TTG AGG GTG CCC AGT GGT CAC	336				
978	Tyr Thr Asp Tyr Cys Asn Arg Ile Asp Leu Arg Val Pro Ser Gly His					
979	100 105 110					
981	CTC AAG GAG CCT GAG CAC CCG TCC ATG TGG GGC CCG GTG GAG CTG GTA	384				
982	Leu Lys Glu Pro Glu His Pro Ser Met Trp Gly Pro Val Glu Leu Val					
983	115 120 125					
985	GGC ATC ATC GCC GGC CCG GTG TTC CTC CTG TTC CTC ATC ATC ATT	432				

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001
TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRF3\10152001\I039177D.raw

986	Gly	Ile	Ile	Ala	Gly	Pro	Val	Phe	Leu	Leu	Phe	Leu	Ile	Ile	Ile		
987	130						135					140					
989	GTT	TTC	CTT	GTC	ATT	AAC	TAT	CAT	CAG	CGT	GTC	TAT	CAC	AAC	CGC	CAG	480
990	Val	Phe	Leu	Val	Ile	Asn	Tyr	His	Gln	Arg	Val	Tyr	His	Asn	Arg	Gln	
991	145						150					155				160	
993	AGA	CTG	GAC	ATG	GAA	GAT	CCC	TCA	TGT	GAG	ATG	TGT	CTC	TCC	AAA	GAC	528
994	Arg	Leu	Asp	Met	Glu	Asp	Pro	Ser	Cys	Glu	Met	Cys	Leu	Ser	Lys	Asp	
995							165					170				175	
997	AAG	ACG	CTC	CAG	GAT	CTT	GTC	TAC	GAT	CTC	TCC	ACC	TCA	GGG	TCT	GGC	576
998	Lys	Thr	Leu	Gln	Asp	Leu	Val	Tyr	Asp	Leu	Ser	Thr	Ser	Gly	Ser	Gly	
999							180					185				190	
1001	TCA	GGG	TTA	CCC	CTC	TTT	GTC	CAG	CGC	ACA	GTG	GCC	CGA	ACC	ATC	GTT	624
1002	Ser	Gly	Leu	Pro	Leu	Phe	Val	Gln	Arg	Thr	Val	Ala	Arg	Thr	Ile	Val	
1003							195					200				205	
1005	TTA	CAA	GAG	ATT	ATT	GGC	AAG	GGT	CGG	TTT	GGG	GAA	GTA	TGG	CGG	GGC	672
1006	Leu	Gln	Glu	Ile	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	Val	Trp	Arg	Gly	
1007							210					215				220	
1009	CGC	TGG	AGG	GGT	GGT	GAT	GTC	GCT	GTG	AAA	ATA	TTC	TCT	TCT	CGT	GAA	720
1010	Arg	Trp	Arg	Gly	Gly	Asp	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Glu	
1011	225						230					235				240	
1013	GAA	CGG	TCT	TGG	TTC	AGG	GAA	GCA	GAG	ATA	TAC	CAG	ACG	GTC	ATG	CTG	768
1014	Glu	Arg	Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	Val	Met	Leu	
1015							245					250				255	
1016	CGC	CAT	GAA	AAC	ATC	CTT	GGA	TTT	ATT	GCT	GCT	GAC	AAT	AAA	GAT	AAT	816
1017	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn	Lys	Asp	Asn	
1018							260					265				270	
1020	GGC	ACC	TGG	ACA	CAG	CTG	TGG	CTT	GTT	TCT	GAC	TAT	CAT	GAG	CAC	GGG	864
1021	Gly	Thr	Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	His	Glu	His	Gly	
1022							275					280				285	
1024	TCC	CTG	TTT	GAT	TAT	CTG	AAC	CGG	TAC	ACA	GTG	ACA	ATT	GAG	GGG	ATG	912
1025	Ser	Leu	Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	Thr	Ile	Glu	Gly	Met	
1026							290					295				300	
1028	ATT	AAG	CTG	GCC	TTG	TCT	GCT	AGT	GGG	CTG	GCA	CAC	CTG	CAC	ATG	960	
1029	Ile	Lys	Leu	Ala	Leu	Ser	Ala	Ala	Ser	Gly	Leu	Ala	His	Leu	His	Met	
1030	305						310					315				320	
1032	GAG	ATC	GTG	GGC	ACC	CAA	GGG	AAG	CCT	GGA	ATT	GCT	CAT	CGA	GAC	TTA	1008
1033	Glu	Ile	Val	Gly	Thr	Gln	Gly	Lys	Pro	Gly	Ile	Ala	His	Arg	Asp	Leu	
1034							325					330				335	
1036	AAG	TCA	AAG	AAC	ATT	CTG	GTG	AAG	AAA	AAT	GGC	ATG	TGT	GCC	ATA	GCA	1056
1037	Lys	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Met	Cys	Ala	Ile	Ala	
1038							340					345				350	
1040	GAC	CTG	GGC	CTG	GCT	GTC	CGT	CAT	GAT	GCA	GTC	ACT	GAC	ACC	ATT	GAC	1104
1041	Asp	Leu	Gly	Leu	Ala	Val	Arg	His	Asp	Ala	Val	Thr	Asp	Thr	Ile	Asp	
1042							355					360				365	
1044	ATT	GCC	CCG	AAT	CAG	AGG	GTG	GGG	ACC	AAA	CGA	TAC	ATG	GCC	CCT	GAA	1152
1045	Ile	Ala	Pro	Asn	Gln	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	
1046							370					375				380	
1048	GTA	CTT	GAT	GAA	ACC	ATT	AAT	ATG	AAA	CAC	TTT	GAC	TCC	TTT	AAA	TGT	1200
1049	Val	Leu	Asp	Glu	Thr	Ile	Asn	Met	Lys	His	Phe	Asp	Ser	Phe	Lys	Cys	

RAW SEQUENCE LISTING DATE: 10/15/2001
 PATENT APPLICATION: US/09/039,177D TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
 Output Set: N:\CRF3\10152001\I039177D.raw

1050	385	390	395	400	
1052	GCT GAT ATT TAT GCC CTC GGG CTT GTA TAT TGG GAG ATT GCT CGA AGA				1248
1053	Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg				
1054	405	410	415		
1056	TGC AAT TCT GGA GGA GTC CAT GAA GAA TAT CAG CTG CCA TAT TAC GAC				1296
1057	Cys Asn Ser Gly Gly Val His Glu Glu Tyr Gln Leu Pro Tyr Tyr Asp				
1058	420	425	430		
1060	TTA GTG CCC TCT GAC CCT TCC ATT GAG GAA ATG CGA AAG GTT GTA TGT				1344
1061	Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys				
1062	435	440	445		
1064	GAT CAG AAG CTG CGT CCC AAC ATC CCC AAC TGG TGG CAG AGT TAT GAG				1392
1065	Asp Gln Lys Leu Arg Pro Asn Ile Pro Asn Trp Trp Gln Ser Tyr Glu				
1066	450	455	460		
1068	GCA CTG CGG GTG ATG GGG AAG ATG ATG CGA GAG TGT TGG TAT GCC AAC				1440
1069	Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn				
1070	465	470	475	480	
1072	GGC GCA GCC CGC CTG ACG GCC CTG CGC ATC AAG AAG ACC CTC TCC CAG				1488
1073	Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln				
1074	485	490	495		
1076	CTC AGC GTG CAG GAA GAC GTG AAG ATC TAACTGCTCC CTCTCTCCAC				1535
1077	Leu Ser Val Gln Glu Asp Val Lys Ile				
1078	500	505			
E-->	1080 ACGGAGCTCC TGGCAGCGAG AACTACGCAC AGCTGCCGCG TTGAGCGTAC				
	1081 GATGGAGGCC 1595				
E-->	1083 TACCTCTCGT TTCTGCCAG CCCTCTGTGG CCAGGAGCCC TGGCCCGCAA				
	1084 GAGGGACACA 1655				
E-->	1086 GCCCGGGAGA GACTCGCTCA CTCCCATGTT GGGTTGAGA CAGACACCTT				
	1087 TTCTATTAC 1715				
E-->	1089 CTCCTAATGG CATGGAGACT CTGAGAGCGA ATTGTGTGGA GAACTCAGTG				
	1090 CCACACCTCG 1775				
E-->	1092 AACTGGTTGT AGTGGGAAGT CCCCGAAAC CCGGTGCATC TGGCACGTGG				
	1093 CCAGGAGCCA 1835				
E-->	1095 TGACAGGGGC GCTTGGGAGG GGCGGGAGGA ACCGAGGTGT TGCCAGTGCT				
	1096 AAGCTGCCCT 1895				
E-->	1098 GAGGGTTTCC TTCGGGGACC AGCCCACAGC ACACCAAGGT GGCCCGGAAG				
	1099 AACCAGAAGT 1955				
E-->	1101 GCAGCCCCTC TCACAGGCAG CTCTGAGCCG CGCTTCCCC TCCTCCCTGG				
	1102 GATGGACGCT 2015				
E-->	1104 GCCGGGAGAC TGCCAGTGG ACGGAATCT GCCGTTTGT CTGTCCAGCC				
	1105 GTGTGTGCAT 2075				
E-->	1107 GTGCCGAGGT GCGTCCCCCG TTGTGCCCTGG TTCTGCCAT GCCCTTACAC				
	1108 GTGCGTGTGA 2135				
E-->	1110 GTGTGTGTGT GTGTCTGTAG GTGCGCACTT ACCTGCTTGA GCTTTCTGTG				
	1111 CATGTGCAGG 2195				
E-->	1113 TCGGGGGTGT GGTGGTCATG CTGTCCGTGC TTGCTGGTGC CTCTTTCA				
	1114 TAGTGAGCAG 2255				
E-->	1116 CATCTAGTTT CCCTGGTGCC CTTCCCTGGA GGTCTCTCCC TCCCCCAGAG				
	1117 CCCCTCATGC 2315				
	1119 CACAGTGGTA CTCTGTGT 2333				

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001
TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRF3\10152001\I039177D.raw

1199 (2) INFORMATION FOR SEQ ID NO: 9:
1200 (i) SEQUENCE CHARACTERISTICS:
1201 (A) LENGTH: 2308 base pairs
1202 (B) TYPE: nucleic acid
1203 (C) STRANDEDNESS: unknown
1204 (D) TOPOLOGY: linear
1206 (ii) MOLECULE TYPE: cDNA
1208 (iii) HYPOTHETICAL: NO
C--> 1210 (iv) ANTI-SENSE: NO
1212 (v) FRAGMENT TYPE: internal
1214 (vi) ORIGINAL SOURCE:
1215 (A) ORGANISM: Mouse
1217 (ix) FEATURE:
1218 (A) NAME/KEY: CDS
1219 (B) LOCATION: 77..1585
1221 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

E--> 1223 GGCAGGGCGA GGTTGCTGG GGTGAGGCAG CGGCGCGGCC GGGCCGGGCC

1224 GGGCCACAGG 60

E--> 1226 CGGTGGCGGC GGGACC ATG GAG GCG GCG GTC GCT GCT CCG CGT CCC CGG

W--> 1227 109

1228	Met	Glu	Ala	Ala	Val	Ala	Ala	Pro	Arg	Pro	Arg						
1229			1			5				10							
1231	CTG	CTC	CTC	GTG	CTG	GCG	GCG	GCG	GCG	GCG	GCG	CTG	157				
1232	Leu	Leu	Leu	Leu	Val	Leu	Ala	Ala	Ala	Ala	Ala	Ala					
1233						15		20		25							
1235	CTC	CCG	GGG	GCG	ACG	GCG	TTA	CAG	TGT	TTC	TGC	CAC	CTC	TGT	ACA	AAA	205
1236	Leu	Pro	Gly	Ala	Thr	Ala	Leu	Gln	Cys	Phe	Cys	His	Leu	Cys	Thr	Lys	
1237						30		35			40						
1239	GAC	AAT	TTT	ACT	TGT	GTG	ACA	GAT	GGG	CTC	TGC	TTT	GTC	TCT	GTC	ACA	253
1240	Asp	Asn	Phe	Thr	Cys	Val	Thr	Asp	Gly	Leu	Cys	Phe	Val	Ser	Val	Thr	
1241						45		50			55						
1243	GAG	ACC	ACA	GAC	AAA	GTT	ATA	CAC	AAC	AGC	ATG	TGT	ATA	GCT	GAA	ATT	301
1244	Glu	Thr	Thr	Asp	Lys	Val	Ile	His	Asn	Ser	Met	Cys	Ile	Ala	Glu	Ile	
1245						60		65			70			75			
1247	GAC	TTA	ATT	CCT	CGA	GAT	AGG	CCG	TTT	GTA	TGT	GCA	CCC	TCT	TCA	AAA	349
1248	Asp	Leu	Ile	Pro	Arg	Asp	Arg	Pro	Phe	Val	Cys	Ala	Pro	Ser	Ser	Lys	
1249						80			85			90					
1251	ACT	GGG	TCT	GTG	ACT	ACA	ACA	TAT	TGC	TGC	AAT	CAG	GAC	CAT	TGC	AAT	397
1252	Thr	Gly	Ser	Val	Thr	Thr	Thr	Tyr	Cys	Cys	Asn	Gln	Asp	His	Cys	Asn	
1253						95			100			105					
1255	AAA	ATA	GAA	CTT	CCA	ACT	ACT	GTA	AAG	TCA	TCA	CCT	GGC	CTT	GGT	CCT	445
1256	Lys	Ile	Glu	Leu	Pro	Thr	Thr	Val	Lys	Ser	Ser	Pro	Gly	Leu	Gly	Pro	
1257						110		115			120						
1259	GTG	GAA	CTG	GCA	GCT	GTC	ATT	GCT	GGA	CCA	GTG	TGC	TTC	GTC	TGC	ATC	493
1260	Val	Glu	Leu	Ala	Ala	Val	Ile	Ala	Gly	Pro	Val	Cys	Phe	Val	Cys	Ile	
1261						125		130			135						
1263	TCA	CTC	ATG	TTG	ATG	GTC	TAT	ATC	TGC	CAC	AAC	CGC	ACT	GTC	ATT	CAC	541
1264	Ser	Leu	Met	Leu	Met	Val	Tyr	Ile	Cys	His	Asn	Arg	Thr	Val	Ile	His	
1265	140					145			150			155					

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001
TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRF3\10152001\I039177D.raw

1267 CAT CGA GTG CCA AAT GAA GAG GAC CCT TCA TTA GAT CGC CCT TTT ATT	589
1268 His Arg Val Pro Asn Glu Glu Asp Pro Ser Leu Asp Arg Pro Phe Ile	
1269 160 165 170	
1271 TCA GAG GGT ACT ACG TTG AAA GAC TTA ATT TAT GAT ATG ACA ACG TCA	637
1272 Ser Glu Gly Thr Thr Leu Lys Asp Leu Ile Tyr Asp Met Thr Thr Ser	
1273 175 180 185	
1275 GGT TCT GGC TCA GGT TTA CCA TTG CTT GTT CAG AGA ACA ATT GCG AGA	685
1276 Gly Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Arg	
1277 190 195 200	
1279 ACT ATT GTG TTA CAA GAA AGC ATT GGC AAA GGT CGA TTT GGA GAA GTT	733
1280 Thr Ile Val Leu Gln Glu Ser Ile Gly Lys Gly Arg Phe Gly Glu Val	
1281 205 210 215	
1283 TGG AGA GGA AAG TGG CGG GGA GAA GAA GTT GCT GTT AAG ATA TTC TCC	781
1284 Trp Arg Gly Lys Trp Arg Gly Glu Glu Val Ala Val Lys Ile Phe Ser	
1285 220 225 230 235	
1287 TCT AGA GAA GAA CGT TCG TGG TTC CGT GAG GCA GAG ATT TAT CAA ACT	829
1288 Ser Arg Glu Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr	
1289 240 245 250	
1291 GTA ATG TTA CGT CAT GAA AAC ATC CTG GGA TTT ATA GCA GCA GAC AAT	877
1292 Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn	
1293 255 260 265	
1295 AAA GAC AAT GGT ACT TGG ACT CAG CTC TGG TTG GTG TCA GAT TAT CAT	925
1296 Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His	
1297 270 275 280	
1299 GAG CAT GGA TCC CTT TTT GAT TAC TTA AAC AGA TAC ACA GTT ACT GTG	973
1300 Glu His Gly Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Val	
1301 285 290 295	
1303 GAA GGA ATG ATA AAA CTT GCT CTG TCC ACG GCG AGC GGT CTT GCC CAT	1021
1304 Glu Gly Met Ile Lys Leu Ala Leu Ser Thr Ala Ser Gly Leu Ala His	
1305 300 305 310 315	
1307 CTT CAC ATG GAG ATT GTT GGT ACC CAA GGA AAG CCA GCC ATT GCT CAT	1069
1308 Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Ala Ile Ala His	
1309 320 325 330	
1311 AGA GAT TTG AAA TCA AAG AAT ATC TTG GTA AAG AAG AAT GGA ACT TGC	1117
1312 Arg Asp Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys	
1313 335 340 345	
1315 TGT ATT GCA GAC TTA GGA CTG GCA GTA AGA CAT GAT TCA GCC ACA GAT	1165
1316 Cys Ile Ala Asp Leu Gly Leu Ala Val Arg His Asp Ser Ala Thr Asp	
1317 350 355 360	
1319 ACC ATT GAT ATT GCT CCA AAC CAC AGA GTG GGA ACA AAA AGG TAC ATG	1213
1320 Thr Ile Asp Ile Ala Pro Asn His Arg Val Gly Thr Lys Arg Tyr Met	
1321 365 370 375	
1323 GCC CCT GAA GTT CTC GAT GAT TCC ATA AAT ATG AAA CAT TTT GAA TCC	1261
1324 Ala Pro Glu Val Leu Asp Asp Ser Ile Asn Met Lys His Phe Glu Ser	
1325 380 385 390 395	
1327 TTC AAA CGT GCT GAC ATC TAT GCA ATG GGC TTA GTA TTC TGG GAA ATT	1309
1328 Phe Lys Arg Ala Asp Ile Tyr Ala Met Gly Leu Val Phe Trp Glu Ile	
1329 400 405 410	
1331 GCT CGA CGA TGT TCC ATT GGT GGA ATT CAT GAA GAT TAC CAA CTG CCT	1357

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001

TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
 Output Set: N:\CRF3\10152001\I039177D.raw

1332 Ala Arg Arg Cys Ser Ile Gly Gly Ile His Glu Asp Tyr Gln Leu Pro
 1333 415 420 425
 1335 TAT TAT GAT CTT GTA CCT TCT GAC CCA TCA GTT GAA GAA ATG AGA AAA 1405
 1336 Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Val Glu Glu Met Arg Lys
 1337 430 435 440
 1339 GTT GTT TGT GAA CAG AAG TTA AGG CCA AAT ATC CCA AAC AGA TGG CAG 1453
 1340 Val Val Cys Glu Gln Lys Leu Arg Pro Asn Ile Pro Asn Arg Trp Gln
 1341 445 450 455
 1343 AGC TGT GAA GCC TTG AGA GTA ATG GCT AAA ATT ATG AGA GAA TGT TGG 1501
 1344 Ser Cys Glu Ala Leu Arg Val Met Ala Lys Ile Met Arg Glu Cys Trp
 1345 460 465 470 475
 1347 TAT GCC AAT GGA GCA GCT AGG CTT ACA GCA TTG CGG ATT AAG AAA ACA 1549
 1348 Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr
 1349 480 485 490
 1351 TTA TCG CAA CTC AGT CAA CAG GAA GGC ATC AAA ATG TAATTCTACA 1595
 1352 Leu Ser Gln Leu Ser Gln Gln Glu Gly Ile Lys Met
 1353 495 500
 E--> 1355 GCTTGCCCTG AACTCTCCTT TTTTCTTCAG ATCTGCTCCT GGGTTTTAAT
 1356 TTGGGAGGTC 1655
 E--> 1358 AGTTGTTCTA CCTCACTGAG AGGGAACAGA AGGATATTGC TTCCTTTGC
 1359 AGCAGTGTAA 1715
 E--> 1361 TAAAGTCAT TAAAAACTTC CCAGGATTTCC TTTGGACCCA GGAAACAGCC
 1362 ATGTGGGTCC 1775
 E--> 1364 TTTCTGTGCA CTATGAACGC TTCTTTCCA GGACAGAAAA TGTGTAGTCT
 1365 ACCTTTATTT 1835
 E--> 1367 TTTATTAACA AAACCTGTTT TTTAAAAAGA TGATTGCTGG TCTTAACCTT
 1368 AGGTAACCT 1895
 E--> 1370 GCTGTGCTGG AGATCATCTT TAAGGGAAA GGAGTTGGAT TGCTGAATTA
 1371 CAATGAAACA 1955
 E--> 1373 TGTCTTATTA CTAAAGAAAG TGATTTACTC CTGGTTAGTA CATTCTCAGA
 1374 GGATTCTGAA 2015
 E--> 1376 CCACTAGAGT TTCCCTGATT CAGACTTGA ATGTACTGTT CTATAGTTT
 1377 TCAGGATCTT 2075
 E--> 1379 AAAACTAACCA CTTATAAAAC TCTTATCTTG AGTCTAAAAA TGACCTCATA
 1380 TAGTAGTGAG 2135
 E--> 1382 GAACATAATT CATGCAATTG TATTTGTAT ACTATTATTG TTCTTTCACT
 1383 TATTCAAGAAC 2195
 E--> 1385 ATTACATGCC TTCAAAATGG GATTGTACTA TACCAAGTAAG TGCCACTTCT
 1386 GTGTCTTTCT 2255
 E--> 1388 AATGGAAATG AGTAGAATTG CTGAAAGTCT CTATGTTAAA ACCTATAGTG TTT
 W--> 1389 2308
 1468 (2) INFORMATION FOR SEQ ID NO: 11:
 1469 (i) SEQUENCE CHARACTERISTICS:
 1470 (A) LENGTH: 1922 base pairs
 1471 (B) TYPE: nucleic acid
 1472 (C) STRANDEDNESS: unknown
 1473 (D) TOPOLOGY: linear
 1475 (ii) MOLECULE TYPE: cDNA
 1477 (iii) HYPOTHETICAL: NO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001
TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRF3\10152001\I039177D.raw

C--> 1479 (iv) ANTI-SENSE: NO
1481 (v) FRAGMENT TYPE: internal
1483 (vi) ORIGINAL SOURCE:
1484 (A) ORGANISM: Mouse
1486 (ix) FEATURE:
1487 (A) NAME/KEY: CDS
1488 (B) LOCATION: 241..1746
1490 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
E--> 1492 GAGAGCACAG CCCTTCCCAG TCCCCGGAGC CGCCGCGCCA CGCGCGCATG
1493 ATCAAGACTT 60
E--> 1495 TTTCCCCGGC CCCACAGGGC CTCTGGACGT GAGACCCCGG CCGCCTCCGC
1496 AAGGAGAGGC 120
E--> 1498 GGGGGTCGAG TCGCCCTGTC CAAAGGCCTC AATCTAAACA ATCTTGATTC
1499 CTGTTGCCGG 180
E--> 1501 CTGGCGGGAC CCTGAATGGC AGGAAATCTC ACCACATCTC TTCTCCATTC
1502 TCCAAGGACC 240
1504 ATG ACC TTG GGG AGC TTC AGA AGG GGC CTT TTG ATG CTG TCG GTG GCC 288
1505 Met Thr Leu Gly Ser Phe Arg Arg Gly Leu Leu Met Leu Ser Val Ala
1506 1 5 10 15
1508 TTG GGC CTA ACC CAG GGG AGA CTT GCG AAG CCT TCC AAG CTG GTG AAC 336
1509 Leu Gly Leu Thr Gln Gly Arg Leu Ala Lys Pro Ser Lys Leu Val Asn
1510 20 25 30
1512 TGC ACT TGT GAG AGC CCA CAC TGC AAG AGA CCA TTC TGC CAG GGG TCA 384
1513 Cys Thr Cys Glu Ser Pro His Cys Lys Arg Pro Phe Cys Gln Gly Ser
1514 35 40 45
1516 TGG TGC ACA GTG GTG CTG GTT CGA GAG CAG GGC AGG CAC CCC CAG GTC 432
1517 Trp Cys Thr Val Val Leu Val Arg Glu Gln Gly Arg His Pro Gln Val
1518 50 55 60
1520 TAT CGG GGC TGT GGG AGC CTG AAC CAG GAG CTC TGC TTG GGA CGT CCC 480
1521 Tyr Arg Gly Cys Gly Ser Leu Asn Gln Glu Leu Cys Leu Gly Arg Pro
1522 65 70 75 80
1524 ACG GAG TTT CTG AAC CAT CAC TGC TGC TAT AGA TCC TTC TGC AAC CAC 528
1525 Thr Glu Phe Leu Asn His His Cys Cys Tyr Arg Ser Phe Cys Asn His
1526 85 90 95
1528 AAC GTG TCT CTG ATG CTG GAG GCC ACC CAA ACT CCT TCG GAG GAG CCA 576
1529 Asn Val Ser Leu Met Leu Glu Ala Thr Gln Thr Pro Ser Glu Glu Pro
1530 100 105 110
1532 GAA GTT GAT GCC CAT CTG CCT CTG ATC CTG GGT CCT GTG CTG GCC TTG 624
1533 Glu Val Asp Ala His Leu Pro Leu Ile Leu Gly Pro Val Leu Ala Leu
1534 115 120 125
1536 CCG GTC CTG GTG GCC CTG GGT GCT CTG GGC TTG TGG CGT GTC CGG CGG 672
1537 Pro Val Leu Val Ala Leu Gly Ala Leu Gly Leu Trp Arg Val Arg Arg
1538 130 135 140
1540 AGG CAG GAG AAG CAG CGG GAT TTG CAC AGT GAC CTG GGC GAG TCC AGT 720
1541 Arg Gln Glu Lys Gln Arg Asp Leu His Ser Asp Leu Gly Glu Ser Ser
1542 145 150 155 160
1544 CTC ATC CTG AAG GCA TCT GAA CAG GCA GAC AGC ATG TTG GGG GAC TTC 768
1545 Leu Ile Leu Lys Ala Ser Glu Gln Ala Asp Ser Met Leu Gly Asp Phe
1546 165 170 175

RAW SEQUENCE LISTING DATE: 10/15/2001
 PATENT APPLICATION: US/09/039,177D TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
 Output Set: N:\CRF3\10152001\I039177D.raw

1548	CTG	GAC	AGC	GAC	TGT	ACC	ACG	GGC	AGC	GGC	TCG	GGG	CTC	CCC	TTC	TTG	816
1549	Leu	Asp	Ser	Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe	Leu	
1550									180		185					190	
1552	GTG	CAG	AGG	ACG	GTA	GCT	CGG	CAG	GTT	GCG	CTG	GTA	GAG	TGT	GTG	GGA	864
1553	Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Val	Ala	Leu	Val	Glu	Cys	Val	Gly	
1554									195		200					205	
1556	AAG	GGC	CGA	TAT	GGC	GAG	GTG	TGG	CGC	GGT	TCG	TGG	CAT	GGC	GAA	AGC	912
1557	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Ser	Trp	His	Gly	Glu	Ser	
1558									210		215					220	
1560	GTG	GCG	GTC	AAG	ATT	TTC	TCC	TCA	CGA	GAT	GAG	CAG	TCC	TGG	TTC	CGG	960
1561	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Gln	Ser	Trp	Phe	Arg	
1562									225		230					240	
1564	GAG	ACG	GAG	ATC	TAC	AAC	ACA	GTT	CTG	CTT	AGA	CAC	GAC	AAC	ATC	CTA	1008
1565	Glu	Thr	Glu	Ile	Tyr	Asn	Thr	Val	Leu	Leu	Arg	His	Asp	Asn	Ile	Leu	
1566									245		250					255	
1568	GGC	TTC	ATC	GCC	TCC	GAC	ATG	ACT	TCG	CGG	AAC	TCG	AGC	ACG	CAG	CTG	1056
1569	Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser	Arg	Asn	Ser	Ser	Thr	Gln	Leu	
1570									260		265					270	
1572	TGG	CTC	ATC	ACC	CAC	TAC	CAT	GAA	CAC	GGC	TCC	CTC	TAT	GAC	TTT	CTG	1104
1573	Trp	Leu	Ile	Thr	His	Tyr	His	Glu	His	Gly	Ser	Leu	Tyr	Asp	Phe	Leu	
1574									275		280					285	
1576	CAG	AGG	CAG	ACG	CTG	GAG	CCC	CAG	TTG	GCC	CTG	AGG	CTA	GCT	GTG	TCC	1152
1577	Gln	Arg	Gln	Thr	Leu	Glu	Pro	Gln	Leu	Ala	Leu	Arg	Leu	Ala	Val	Ser	
1578									290		295					300	
1580	CCG	GCC	TGC	GGC	CTG	GCG	CAC	CTA	CAT	GTG	GAG	ATC	TTT	GGC	ACT	CAA	1200
1581	Pro	Ala	Cys	Gly	Leu	Ala	His	Leu	His	Val	Glu	Ile	Phe	Gly	Thr	Gln	
1582									305		310					320	
1584	GGC	AAA	CCA	GCC	ATT	GCC	CAT	CGT	GAC	CTC	AAG	AGT	CGC	AAT	GTG	CTG	1248
1585	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Arg	Asn	Val	Leu	
1586									325		330					335	
1588	GTC	AAG	AGT	AAC	TTG	CAG	TGT	TGC	ATT	GCA	GAC	CTG	GGA	CTG	GCT	GTG	1296
1589	Val	Lys	Ser	Asn	Leu	Gln	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val	
1590									340		345					350	
1592	ATG	CAC	TCA	CAA	AGC	AAC	GAG	TAC	CTG	GAT	ATC	GGC	AAC	ACA	CCC	CGA	1344
1593	Met	His	Ser	Gln	Ser	Asn	Glu	Tyr	Leu	Asp	Ile	Gly	Asn	Thr	Pro	Arg	
1594									355		360					365	
1596	GTG	GGT	ACC	AAA	AGA	TAC	ATG	GCA	CCC	GAG	GTG	CTG	GAT	GAG	CAC	ATC	1392
1597	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	His	Ile	
1598									370		375					380	
1600	CCG	ACA	GAC	TGC	TTT	GAG	TCG	TAC	AAG	TGG	ACA	GAC	ATC	TGG	GCC	TTT	1440
1601	Arg	Thr	Asp	Cys	Phe	Glu	Ser	Tyr	Lys	Trp	Thr	Asp	Ile	Trp	Ala	Phe	
1602									385		390					400	
1604	GGC	CTA	GTG	CTA	TGG	GAG	ATC	GCC	CGG	CGG	ACC	ATC	ATC	AAT	GGC	ATT	1488
1605	Gly	Leu	Val	Leu	Trp	Glu	Ile	Ala	Arg	Arg	Thr	Ile	Ile	Asn	Gly	Ile	
1606									405		410					415	
1608	GTG	GAG	GAT	TAC	AGG	CCA	CCT	TTC	TAT	GAC	ATG	GTA	CCC	AAT	GAC	CCC	1536
1609	Val	Glu	Asp	Tyr	Arg	Pro	Pro	Phe	Tyr	Asp	Met	Val	Pro	Asn	Asp	Pro	
1610									420		425					430	
1612	AGT	TTT	GAG	GAC	ATG	AAA	AAG	GTG	GTG	TGC	GTT	GAC	CAG	ACA	CCC		1584

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001

TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
 Output Set: N:\CRF3\10152001\I039177D.raw

1613	Ser	Phe	Glu	Asp	Met	Lys	Lys	Val	Val	Cys	Val	Asp	Gln	Gln	Thr	Pro			
1614		435						440							445				
1616	ACC	ATC	CCT	AAC	CGG	CTG	GCT	GCA	GAT	CCG	GTC	CTC	TCC	GGG	CTG	GCC	1632		
1617	Thr	Ile	Pro	Asn	Arg	Leu	Ala	Ala	Asp	Pro	Val	Leu	Ser	Gly	Leu	Ala			
1618								450			455			460					
1620	CAG	ATG	ATG	AGA	GAG	TGC	TGG	TAC	CCC	AAC	CCC	TCT	GCT	CGC	CTC	ACC	1680		
1621	Gln	Met	Met	Arg	Glu	Cys	Trp	Tyr	Pro	Asn	Pro	Ser	Ala	Arg	Leu	Thr			
1622	465					470					475				480				
1624	GCA	CTG	CGC	ATA	AAG	AAG	ACA	TTG	CAG	AAG	CTC	AGT	CAC	AAT	CCA	GAG	1728		
1625	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Gln	Lys	Leu	Ser	His	Asn	Pro	Glu			
1626						485				490				495					
1628	AAG	CCC	AAA	GTG	ATT	CAC	TAGCCCAGGG	CCACCCAGGCT	TCCTCTGCCT								1776		
1629	Lys	Pro	Lys	Val	Ile	His													
1630						500													
E-->	1632	AAAGTGTGTG	CTGGGAAAGA	AGACATAGCC	TGTCTGGGT	AAGGGAGTGA													
	1633	AGAGAGTGTG	1836																
E-->	1635	CACGCTGCC	TGTGTGTGCC	TGCTCAGCTT	GCTCCCAGCC	CATCCAGCCA													
	1636	AAAATACAGC	1896																
	1638	TGAGCTGAAA	TTCAAAAAAA	AAAAAA													1922		
	1716	(2)	INFORMATION	FOR	SEQ	ID	NO:	13:											
	1717		(i)	SEQUENCE	CHARACTERISTICS:														
	1718			(A)	LENGTH:	2070	base	pairs											
	1719			(B)	TYPE:	nucleic	acid												
	1720			(C)	STRANDEDNESS:	unknown													
	1721			(D)	TOPOLOGY:	linear													
	1723			(ii)	MOLECULE	TYPE:	cDNA												
	1725			(iii)	HYPOTHETICAL:	NO													
C-->	1727			(iv)	ANTI-SENSE:	NO													
	1729			(v)	FRAGMENT	TYPE:	internal												
	1731			(vi)	ORIGINAL	SOURCE:													
	1732				(A)	ORGANISM:	Mouse												
	1734			(ix)	FEATURE:														
	1735				(A)	NAME/KEY:	CDS												
	1736				(B)	LOCATION:	217..1812												
	1738				(xi)	SEQUENCE	DESCRIPTION:	SEQ	ID	NO:	13:								
E-->	1740	ATTCATGAGA	TGGAAGCATA	GGTCAAAGCT	GTTCGGAGAA	ATTGGAACTA													
	1741	CAGTTTATC	60																
E-->	1743	TAGCCACATC	TCTGAGAATT	CTGAAGAAAG	CAGCAGGTGA	AAGTCATTGC													
	1744	CAAGTGATT	120																
E-->	1746	TGTTCTGTAA	GGAAGCCTCC	CTCATTCACT	TACACCAGTG	AGACAGCAGG													
	1747	ACCAGTCATT	180																
E-->	1749	CAAAGGGCCG	TGTACAGGAC	GC GTGGCAAT	CAGACA	ATG ACT CAG CTA TAC ACT													
W-->	1750	234																	
	1751						Met	Thr	Gln	Leu	Tyr	Thr							
	1752							1				5							
	1754	TAC	ATC	AGA	TTA	CTG	GGA	GCC	TGT	CTG	TTC	ATC	ATT	TCT	CAT	GTT	CAA	282	
	1755	Tyr	Ile	Arg	Leu	Leu	Gly	Ala	Cys	Leu	Phe	Ile	Ile	Ser	His	Val	Gln		
	1756					10				15				20					
	1758	GGG	CAG	AAT	CTA	GAT	AGT	ATG	CTC	CAT	GGC	ACT	GGT	ATG	AAA	TCA	GAC	330	

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001
TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRF3\10152001\I039177D.raw

1759	Gly	Gln	Asn	Leu	Asp	Ser	Met	Leu	His	Thr	Gly	Met	Lys	Ser	Asp			
1760	25						30					35						
1762	TTG	GAC	CAG	AAG	AAG	CCA	GAA	AAT	GGA	GTG	ACT	TTA	GCA	CCA	GAG	GAT	378	
1763	Leu	Asp	Gln	Lys	Lys	Pro	Glu	Asn	Gly	Val	Thr	Leu	Ala	Pro	Glu	Asp		
1764	40						45					50						
1766	ACC	TTG	CCT	TTC	TTA	AAG	TGC	TAT	TGC	TCA	GGA	CAC	TGC	CCA	GAT	GAT	426	
1767	Thr	Leu	Pro	Phe	Leu	Lys	Cys	Tyr	Cys	Ser	Gly	His	Cys	Pro	Asp	Asp		
1768	55					60				65			70					
1770	GCT	ATT	AAT	AAC	ACA	TGC	ATA	ACT	AAT	GGC	CAT	TGC	TTT	GCC	ATT	ATA	474	
1771	Ala	Ile	Asn	Asn	Thr	Cys	Ile	Thr	Asn	Gly	His	Cys	Phe	Ala	Ile	Ile		
1772						75				80			85					
1774	GAA	GAA	GAT	GAT	CAG	GGA	GAA	ACC	ACA	TTA	ACT	TCT	GGG	TGT	ATG	AAG	522	
1775	Glu	Glu	Asp	Asp	Gln	Gly	Glu	Thr	Thr	Leu	Thr	Ser	Gly	Cys	Met	Lys		
1776					90			95					100					
1778	TAT	GAA	GGC	TCT	GAT	TTT	CAA	TGC	AAG	GAT	TCA	CCG	AAA	GCC	CAG	CTA	570	
1779	Tyr	Glu	Gly	Ser	Asp	Phe	Gln	Cys	Lys	Asp	Ser	Pro	Lys	Ala	Gln	Leu		
1780					105			110					115					
1782	CGC	AGG	ACA	ATA	GAA	TGT	TGT	CGG	ACC	AAT	TTG	TGC	AAC	CAG	TAT	TTG	618	
1783	Arg	Arg	Thr	Ile	Glu	Cys	Cys	Arg	Thr	Asn	Leu	Cys	Asn	Gln	Tyr	Leu		
1784					120			125				130						
1786	CAG	CCT	ACA	CTG	CCC	CCC	CCT	GTT	GTT	ATA	GGT	CCG	TTC	TTT	GAT	GGC	AGC	666
1787	Gln	Pro	Thr	Leu	Pro	Pro	Val	Val	Ile	Gly	Pro	Phe	Phe	Asp	Gly	Ser		
1788					135			140			145			150				
1790	ATC	CGA	TGG	CTG	GTT	GTT	GTG	CTC	ATT	TCC	ATG	GCT	GTC	TGT	ATA	GTT	GCT	714
1791	Ile	Arg	Trp	Leu	Val	Val	Leu	Ile	Ser	Met	Ala	Val	Cys	Ile	Val	Ala		
1792					155					160			165					
1794	ATG	ATC	ATC	TTC	TCC	AGC	TGC	TTT	TGC	TAT	AAG	CAT	TAT	TGT	AAG	AGT	762	
1795	Met	Ile	Ile	Phe	Ser	Ser	Cys	Phe	Cys	Tyr	Lys	His	Tyr	Cys	Lys	Ser		
1796					170				175			180						
1798	ATC	TCA	AGC	AGG	GGT	CGT	TAC	AAC	CGT	GAT	TTG	GAA	CAG	GAT	GAA	GCA	810	
1799	Ile	Ser	Ser	Arg	Gly	Arg	Tyr	Asn	Arg	Asp	Leu	Glu	Gln	Asp	Glu	Ala		
1800					185			190			195							
1802	TTT	ATT	CCA	GTA	GGA	GAA	TCA	TTG	AAA	GAC	CTG	ATT	GAC	CAG	TCC	CAA	858	
1803	Phe	Ile	Pro	Val	Gly	Glu	Ser	Leu	Lys	Asp	Leu	Ile	Asp	Gln	Ser	Gln		
1804					200			205			210							
1806	AGC	TCT	GGG	AGT	GGA	TCT	GGA	TTG	CCT	TTA	TTG	GTT	CAG	CGA	ACT	ATT	906	
1807	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile		
1808					215			220			225			230				
1810	GCC	AAA	CAG	ATT	CAG	ATG	GTT	CGG	CAG	GTT	GGT	AAA	GGC	CGC	TAT	GGA	954	
1811	Ala	Lys	Gln	Ile	Gln	Met	Val	Arg	Gln	Val	Gly	Lys	Gly	Arg	Tyr	Gly		
1812					235				240			245						
1814	GAA	GTA	TGG	ATG	GGT	AAA	TGG	CGT	GGT	GAA	AAA	GTG	GCT	GTC	AAA	GTG	1002	
1815	Glu	Val	Trp	Met	Gly	Lys	Trp	Arg	Gly	Glu	Lys	Val	Ala	Val	Lys	Val		
1816					250			255			260							
1818	TTT	TTT	ACC	ACT	GAA	GAA	GCT	AGC	TGG	TTT	AGA	GAA	ACA	GAA	ATC	TAC	1050	
1819	Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser	Trp	Phe	Arg	Glu	Thr	Glu	Ile	Tyr		
1820					265			270			275							
1822	CAG	ACG	GTG	TTA	ATG	CGT	CAT	GAA	AAT	ATA	CTT	GGT	TTT	ATA	GCT	GCA	1098	
1823	Gln	Thr	Val	Leu	Met	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala		

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001
TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRF3\10152001\I039177D.raw

1824	280	285	290	
1826	GAC ATT AAA GGC ACT GGT TCC TGG ACT CAG CTG TAT TTG ATT ACT GAT			1146
1827	Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln Leu Tyr Leu Ile Thr Asp			
1828	295	300	305	310
1830	TAC CAT GAA AAT GGA TCT CTC TAT GAC TTC CTG AAA TGT GCC ACA CTA			1194
1831	Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe Leu Lys Cys Ala Thr Leu			
1832	315	320	325	
1834	GAC ACC AGA GCC CTA CTC AAG TTA GCT TAT TCT GCT GCT TGT GGT CTG			1242
1835	Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr Ser Ala Ala Cys Gly Leu			
1836	330	335	340	
1838	TGC CAC CTC CAC ACA GAA ATT TAT GGT ACC CAA GGG AAG CCT GCA ATT			1290
1839	Cys His Leu His Thr Glu Ile Tyr Gly Thr Gln Gly Lys Pro Ala Ile			
1840	345	350	355	
1842	GCT CAT CGA GAC CTG AAG AGC AAA AAC ATC CTT ATT AAG AAA AAT GGA			1338
1843	Ala His Arg Asp Leu Lys Ser Lys Asn Ile Leu Ile Lys Lys Asn Gly			
1844	360	365	370	
1846	AGT TGC TGT ATT GCT GAC CTG GGC CTA GCT GTT AAA TTC AAC AGT GAT			1386
1847	Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Lys Phe Asn Ser Asp			
1848	375	380	385	390
1850	ACA AAT GAA GTT GAC ATA CCC TTG AAT ACC AGG GTG GGC ACC AAG CGG			1434
1851	Thr Asn Glu Val Asp Ile Pro Leu Asn Thr Arg Val Gly Thr Lys Arg			
1852	395	400	405	
1854	TAC ATG GCT CCA GAA GTG CTG GAT GAA AGC CTG AAT AAA AAC CAT TTC			1482
1855	Tyr Met Ala Pro Glu Val Leu Asp Glu Ser Leu Asn Lys Asn His Phe			
1856	410	415	420	
1858	CAG CCC TAC ATC ATG GCT GAC ATC TAT AGC TTT GGT TTG ATC ATT TGG			1530
1859	Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser Phe Gly Leu Ile Ile Trp			
1860	425	430	435	
1862	GAA ATG GCT CGT CGT ATT ACA GGA GGA ATC GTG GAG GAA TAT CAA			1578
1863	Glu Met Ala Arg Arg Cys Ile Thr Gly Gly Ile Val Glu Glu Tyr Gln			
1864	440	445	450	
1866	TTA CCA TAT TAC AAC ATG GTG CCC AGT GAC CCA TCC TAT GAG GAC ATG			1626
1867	Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp Pro Ser Tyr Glu Asp Met			
1868	455	460	465	470
1870	CGT GAG GTT GTG TGT GTG AAA CGC TTG CGG CCA ATC GTG TCT AAC CGC			1674
1871	Arg Glu Val Val Cys Val Lys Arg Leu Arg Pro Ile Val Ser Asn Arg			
1872	475	480	485	
1874	TGG AAC AGC GAT GAA TGT CTT CGA GCA GTT TTG AAG CTA ATG TCA GAA			1722
1875	Trp Asn Ser Asp Glu Cys Leu Arg Ala Val Leu Lys Leu Met Ser Glu			
1876	490	495	500	
1878	TGT TGG GCC CAT AAT CCA GCC TCC AGA CTC ACA GCT TTG AGA ATC AAG			1770
1879	Cys Trp Ala His Asn Pro Ala Ser Arg Leu Thr Ala Leu Arg Ile Lys			
1880	505	510	515	
1882	AAG ACA CTT GCA AAA ATG GTT GAA TCC CAG GAT GTA AAG ATT			1812
1883	Lys Thr Leu Ala Lys Met Val Glu Ser Gln Asp Val Lys Ile			
1884	520	525	530	
E-->	1886 TGACAATTAA ACAATTTGA GGGAGAATT AGACTGCAAG AACTTCTTCA			
	1887 CCCAAGGAAT 1872			
E-->	1889 GGGTGGGATT AGCATGGAAT AGGATGTTGA CTTGGTTCC AGACTCCTTC			

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001

TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
 Output Set: N:\CRF3\10152001\I039177D.raw

1890 CTCTACATCT 1932
 E--> 1892 TCACAGGCTG CTAACAGTAA ACCTTACCGT ACTCTACAGA ATACAAGATT
 1893 GGAACCTTGGA 1992
 E--> 1895 ACTTCAAACA TGTCAATTCTT TATATATGAC AGCTTTGTTT TAATGTGGGG
 1896 TTTTTTGTT 2052
 1898 TGCTTTTTT GTTTGTT 2070
 1981 (2) INFORMATION FOR SEQ ID NO: 15:
 1982 (i) SEQUENCE CHARACTERISTICS:
 1983 (A) LENGTH: 2160 base pairs
 1984 (B) TYPE: nucleic acid
 1985 (C) STRANDEDNESS: unknown
 1986 (D) TOPOLOGY: linear
 1988 (ii) MOLECULE TYPE: cDNA
 1990 (iii) HYPOTHETICAL: NO
 C--> 1992 (iv) ANTI-SENSE: NO
 1994 (v) FRAGMENT TYPE: internal
 1996 (vi) ORIGINAL SOURCE:
 1997 (A) ORGANISM: Mouse
 1999 (ix) FEATURE:
 2000 (A) NAME/KEY: CDS
 2001 (B) LOCATION: 10..1524
 2003 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
 2005 CGCGGTTAC ATG GCG GAG TCG GCC GGA GCC TCC TCC TTC CCC CTT 48
 2006 Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu
 2007 1 5 10
 2009 GTT GTC CTC CTG CTC GCC GGC AGC GGC GGG TCC GGG CCC CGG GGG ATC 96
 2010 Val Val Leu Leu Ala Gly Ser Gly Ser Gly Pro Arg Gly Ile
 2011 15 20 25
 2013 CAG GCT CTG CTG TGT GCG TGC ACC AGC TGC CTA CAG ACC AAC TAC ACC 144
 2014 Gln Ala Leu Leu Cys Ala Cys Thr Ser Cys Leu Gln Thr Asn Tyr Thr
 2015 30 35 40 45
 2017 TGT GAG ACA GAT GGG GCT TGC ATG GTC TCC ATC TTT AAC CTG GAT GGC 192
 2018 Cys Glu Thr Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly
 2019 50 55 60
 2021 GTG GAG CAC CAT GTA CGT ACC TGC ATC CCC AAG GTG GAG CTG GTT CCT 240
 2022 Val Glu His His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro
 2023 65 70 75
 2025 GCT GGA AAG CCC TTC TAC TGC CTG AGT TCA GAG GAT CTG CGC AAC ACA 288
 2026 Ala Gly Lys Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr
 2027 80 85 90
 2029 CAC TGC TGC TAT ATT GAC TTC TGC AAC AAG ATT GAC CTC AGG GTC CCC 336
 2030 His Cys Cys Tyr Ile Asp Phe Cys Asn Lys Ile Asp Leu Arg Val Pro
 2031 95 100 105
 2033 AGC GGA CAC CTC AAG GAG CCT GCG CAC CCC TCC ATG TGG GGC CCT GTG 384
 2034 Ser Gly His Leu Lys Glu Pro Ala His Pro Ser Met Trp Gly Pro Val
 2035 110 115 120 125
 2037 GAG CTG GTC GGC ATC ATC GCC GGC CCC GTC TTC CTC CTC TTC CTT ATC 432
 2038 Glu Leu Val Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile
 2039 130 135 140

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001
TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRF3\10152001\I039177D.raw

2041	ATT ATC ATC GTC TTC CTG GTC ATC AAC TAT CAC CAG CGT GTC TAC CAT	480
2042	Ile Ile Ile Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His	
2043	145 150 155	
2045	AAC CGC CAG AGG TTG GAC ATG GAG GAC CCC TCT TGC GAG ATG TGT CTC	528
2046	Asn Arg Gln Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu	
2047	160 165 170	
2049	TCC AAA GAC AAG ACG CTC CAG GAT CTC GTC TAC GAC CTC TCC ACG TCA	576
2050	Ser Lys Asp Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser	
2051	175 180 185	
2053	GGG TCT GGC TCA GGG TTA CCC CTT TTT GTC CAG CGC ACA GTG GCC CGA	624
2054	Gly Ser Gly Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg	
2055	190 195 200 205	
2057	ACC ATT GTT TTA CAA GAG ATT ATC GGC AAG GGC CGG TTC GGG GAA GTA	672
2058	Thr Ile Val Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val	
2059	210 215 220	
2061	TGG CGT GGT CGC TGG AGG GGT GAC GTG GCT GTG AAA ATC TTC TCT	720
2062	Trp Arg Gly Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser	
2063	225 230 235	
2065	TCT CGT GAA GAA CGG TCT TGG TTC CGT GAA GCA GAG ATC TAC CAG ACC	768
2066	Ser Arg Glu Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr	
2067	240 245 250	
2069	GTC ATG CTG CGC CAT GAA AAC ATC CTT GGC TTT ATT GCT GCT GAC AAT	816
2070	Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn	
2071	255 260 265	
2073	AAA GAT AAT GGC ACC TGG ACC CAG CTG TGG CTT GTC TCT GAC TAT CAC	864
2074	Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His	
2075	270 275 280 285	
2077	GAG CAT GGC TCA CTG TTT GAT TAT CTG AAC CGC TAC ACA GTG ACC ATT	912
2078	Glu His Gly Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile	
2079	290 295 300	
2081	GAG GGA ATG ATT AAG CTA GCC TTG TCT GCA GCC AGT GGT TTG GCA CAC	960
2082	Glu Gly Met Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His	
2083	305 310 315	
2085	CTG CAT ATG GAG ATT GTG GGC ACT CAA GGG AAG CCG GGA ATT GCT CAT	1008
2086	Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His	
2087	320 325 330	
2089	CGA GAC TTG AAG TCA AAG AAC ATC CTG GTG AAA AAA AAT GGC ATG TGT	1056
2090	Arg Asp Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys	
2091	335 340 345	
2093	GCC ATT GCA GAC CTG GGC CTG GCT GTC CGT CAT GAT GCG GTC ACT GAC	1104
2094	Ala Ile Ala Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp	
2095	350 355 360 365	
2097	ACC ATA GAC ATT GCT CCA AAT CAG AGG GTG GGG ACC AAA CGA TAC ATG	1152
2098	Thr Ile Asp Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met	
2099	370 375 380	
2101	GCT CCT GAA GTC CTT GAC GAG ACA ATC AAC ATG AAG CAC TTT GAC TCC	1200
2102	Ala Pro Glu Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser	
2103	385 390 395	
2105	TTC AAA TGT GCC GAC ATC TAT GCC CTC GGG CTT GTC TAC TGG GAG ATT	1248

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001

TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRE3\10152001\I039177D.raw

2106 Phe Lys Cys Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile
 2107 400 405 410
 2109 GCA CGA AGA TGC AAT TCT GGA GGA GTC CAT GAA GAC TAT CAA CTG CCG 1296
 2110 Ala Arg Arg Cys Asn Ser Gly Gly Val His Glu Asp Tyr Gln Leu Pro
 2111 415 420 425
 2113 TAT TAC GAC TTA GTG CCC TCC GAC CCT TCC ATT GAG GAG ATG CGA AAG 1344
 2114 Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys
 2115 430 435 440 445
 2117 GTT GTA TGT GAC CAG AAG CTA CGG CCC AAT GTC CCC AAC TGG TGG CAG 1392
 2118 Val Val Cys Asp Gln Lys Leu Arg Pro Asn Val Pro Asn Trp Trp Gln
 2119 450 455 460
 2121 AGT TAT GAG GCC TTG CGA GTG ATG GGA AAG ATG ATG CGG GAG TGC TGG 1440
 2122 Ser Tyr Glu Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp
 2123 465 470 475
 2125 TAC GCC AAT GGT GCT GCC CGT CTG ACA GCT CTG CGC ATC AAG AAG ACT 1488
 2126 Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr
 2127 480 485 490
 2129 CTG TCC CAG CTA AGC GTG CAG GAA GAT GTG AAG ATT TAAGCTGTTTC 1534
 2130 Leu Ser Gln Leu Ser Val Gln Glu Asp Val Lys Ile
 2131 495 500 505
 2133 CTCTGCCTAC ACAAAAGAACCC TGGGCAGTGA GGATGACTGC AGCCACCGTG
 2134 CAAGCGTCGT 1594
 2136 GGAGGCCTAT CCTCTTGTTT CTGCCCGGCC CTCTGGCAGA GCCCTGGCCT
 2137 GCAAGAGGG 1654
 2139 CAGAGCCTGG GAGACGCGCG CACTCCCCTTT GGGTTTGAGA CAGACACTTT
 2140 TTATATTTAC 1714
 2142 CTCCTGATGG CATGGAGACC TGAGCAAATC ATGTAGTCAC TCAATGCCAC
 2143 AACTCAAAC 1774
 2145 GCTTCAGTGG GAAAGTACAGA GACCCAGTGC ATTGCGTGTG CAGGAGCGTG
 2146 AGGTGCTGGG 1834
 2148 CTCGCCAGGA GCGGGCCCCCA TACCTTGTGG TCCACTGGGC TGCAGGTTTT
 2149 CCTCCAGGG 1894
 2151 CCAGTCAACT GGCATCAAGA TATTGAGAGG AACCGGAAGT TTCTCCCTCC
 2152 TTCCCGTAGC 1954
 2154 AGTCCTGAGC CACACCATCC TTCTCATGGA CATCCGGAGG ACTGCCCTA
 2155 GAGACACAAAC 2014
 2157 CTGCTGCCTG TCTGTCCAGC CAAAGTGGCA TGTGCCGAGG TGTGTCCCCAC
 2158 ATTGTGCCTG 2074
 2160 GTCTGTGCCA CGCCCCGTGTG TGTGTGTGTG TGTGTGAGTG AGTGTGTGTG
 2161 TGTACACTTA 2134
 2163 ACCTGCTTGA GCTTCTGTGC ATGTGT 2160
 2242 (2) INFORMATION FOR SEQ ID NO: 17:
 2243 (i) SEQUENCE CHARACTERISTICS:
 2244 (A) LENGTH: 1952 base pairs
 2245 (B) TYPE: nucleic acid
 2246 (C) STRANDEDNESS: unknown
 2247 (D) TOPOLOGY: unknown
 2249 (ii) MOLECULE TYPE: cDNA
 2251 (iii) HYPOTHETICAL: NO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001
TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRF3\10152001\I039177D.raw

C--> 2253 (iv) ANTI-SENSE: NO
2255 (v) FRAGMENT TYPE: internal
2257 (vi) ORIGINAL SOURCE:
2258 (A) ORGANISM: Mouse
2260 (ix) FEATURE:
2261 (A) NAME/KEY: CDS
2262 (B) LOCATION: 187..1692
2264 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
E--> 2266 AAGCGGCGGC AGAAGTTGCC GGCGTGGTGC TCGTAGTGAG GGCGCGGAGG
2267 ACCCGGGACC 60
E--> 2269 TGGGAAGCGG CGGGCGGGTTA ACTTCGGCTG AATCACAAACC ATTTGGCGCT
2270 GAGCTATGAC 120
E--> 2272 AAGAGAGCAA ACAAAAAGTT AAAGGAGCAA CCCGGCCATA AGTGAAGAGA
2273 GAAGTTTATT 180
2275 GATAAAC ATG CTC TTA CGA AGC TCT GGA AAA TTA AAT GTG GGC ACC AAG 228
2276 Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys
2277 1 5 10
2279 AAG GAG GAT GGA GAG AGT ACA GCC CCC ACC CCT CGG CCC AAG ATC CTA 276
2280 Lys Glu Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu
2281 15 20 25 30
2283 CGT TGT AAA TGC CAC CAC CAC TGT CCG GAA GAC TCA GTC AAC AAT ATC 324
2284 Arg Cys Lys Cys His His Cys Pro Glu Asp Ser Val Asn Asn Ile
2285 35 40 45
2287 TGC AGC ACA GAT GGG TAC TGC TTC ACG ATG ATA GAA GAA GAT GAC TCT 372
2288 Cys Ser Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser
2289 50 55 60
2291 GGA ATG CCT GTT GTC ACC TCT GGA TGT CTA GGA CTA GAA GGG TCA GAT 420
2292 Gly Met Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp
2293 65 70 75
2295 TTT CAA TGT CGT GAC ACT CCC ATT CCT CAT CAA AGA AGA TCA ATT GAA 468
2296 Phe Gln Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu
2297 80 85 90
2299 TGC TGC ACA GAA AGG AAT GAG TGT AAT AAA GAC CTC CAC CCC ACT CTG 516
2300 Cys Cys Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu
2301 95 100 105 110
2303 CCT CCT CTC AAG GAC AGA GAT TTT GTT GAT GGG CCC ATA CAC CAC AAG 564
2304 Pro Pro Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys
2305 115 120 125
2307 GCC TTG CTT ATC TCT GTG ACT GTC TGT AGT TTA CTC TTG GTC CTC ATT 612
2308 Ala Leu Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile
2309 130 135 140
2311 ATT TTA TTC TGT TAC TTC AGG TAT AAA AGA CAA GAA GCC CGA CCT CGG 660
2312 Ile Leu Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg
2313 145 150 155
2315 TAC AGC ATT GGG CTG GAG CAG GAC GAG ACA TAC ATT CCT CCT GGA GAG 708
2316 Tyr Ser Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu
2317 160 165 170
2319 TCC CTG AGA GAC TTG ATC GAG CAG TCT CAG AGC TCG GGA AGT GGA TCA 756
2320 Ser Leu Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001
TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRF3\10152001\I039177D.raw

2321	175	180	185	190	
2323	GGC CTC CCT CTG CTG GTC CAA AGG ACA ATA GCT AAG CAA ATT CAG ATG				804
2324	Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met				
2325	195	200	205		
2327	GTG AAG CAG ATT GGA AAA GGC CGC TAT GGC GAG GTG TGG ATG GGA AAG				852
2328	Val Lys Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys				
2329	210	215	220		
2331	TGG CGT GGA GAA AAG GTG GCT GTG AAA GTG TTC TTC ACC ACG GAG GAA				900
2332	Trp Arg Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu				
2333	225	230	235		
2335	GCC AGC TGG TTC CGA GAG ACT GAG ATA TAT CAG ACG GTC CTG ATG CGG				948
2336	Ala Ser Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg				
2337	240	245	250		
2339	CAT GAG AAT ATT CTG GGG TTC ATT GCT GCA GAT ATC AAA GGG ACT GGG				996
2340	His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly				
2341	255	260	265	270	
2343	TCC TGG ACT CAG TTG TAC CTC ATC ACA GAC TAT CAT GAA AAC GGC TCC				1044
2344	Ser Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser				
2345	275	280	285		
2347	CTT TAT GAC TAT CTG AAA TCC ACC ACC TTA GAC GCA AAG TCC ATG CTG				1092
2348	Leu Tyr Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu				
2349	290	295	300		
2351	AAG CTA GCC TAC TCC TCT GTC AGC GGC CTA TGC CAT TTA CAC ACG GAA				1140
2352	Lys Leu Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu				
2353	305	310	315		
2355	ATC TTT AGC ACT CAA GGC AAG CCA GCA ATC GCC CAT CGA GAC TTG AAA				1188
2356	Ile Phe Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys				
2357	320	325	330		
2359	AGT AAA AAC ATC CTG GTG AAG AAA AAT GGA ACT TGC TGC ATA GCA GAC				1236
2360	Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp				
2361	335	340	345	350	
2363	CTG GGC TTG GCT GTC AAG TTC ATT AGT GAC ACA AAT GAG GTT GAC ATC				1284
2364	Leu Gly Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile				
2365	355	360	365		
2367	CCA CCC AAC ACC CGG GTT GGC ACC AAG CGC TAT ATG CCT CCA GAA GTG				1332
2368	Pro Pro Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val				
2369	370	375	380		
2371	CTG GAC GAG AGC TTG AAT AGA AAC CAT TTC CAG TCC TAC ATT ATG GCT				1380
2372	Leu Asp Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala				
2373	385	390	395		
2375	GAC ATG TAC AGC TTT GGA CTC ATC CTC TGG GAG ATT GCA AGG AGA TGT				1428
2376	Asp Met Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys				
2377	400	405	410		
2379	GTT TCT GGA GGT ATA GTG GAA GAA TAC CAG CTT CCC TAT CAC GAC CTG				1476
2380	Val Ser Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu				
2381	415	420	425	430	
2383	GTG CCC AGT GAC CCT TCT TAT GAG GAC ATG AGA GAA ATT GTG TGC ATG				1524
2384	Val Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met				
2385	435	440	445		

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001
TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRF3\10152001\I039177D.raw

2387	AAG AAG TTA CGG CCT TCA TTC CCC AAT CGA TGG AGC AGT GAT GAG TGT	1572
2388	Lys Lys Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys	
2389	450 455 460	
2391	CTC AGG CAG ATG GGG AAG CTT ATG ACA GAG TGC TGG GCG CAG AAT CCT	1620
2392	Leu Arg Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro	
2393	465 470 475	
2395	GCC TCC AGG CTG ACG GCC CTG AGA GTT AAG AAA ACC CTT GCC AAA ATG	1668
2396	Ala Ser Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met	
2397	480 485 490	
E-->	2399 TCA GAG TCC CAG GAC ATT AAA CTC TGACGTCAGA TACTTGTGGA CAGAGCAAGA	
W-->	2400 1722	
	2401 Ser Glu Ser Gln Asp Ile Lys Leu	
W-->	2402 495 500	
E-->	2404 ATTTCACAGA AGCATCGTTA GCCCAAGCCT TGAAACGTTAG CCTACTGCC	
	2405 AGTGAGTTCA 1782	
E-->	2407 GACTTTCTG GAAGAGAGCA CGGTGGGCAG ACACAGAGGA ACCCAGAAAC	
	2408 ACGGATTCAT 1842	
E-->	2410 CATGGCTTTC TGAGGGAGGAG AAACTGTTG GGTAACTTGT TCAAGATATG	
	2411 ATGCATGTTG 1902	
	2413 CTTTCTAAGA AAGCCCTGTA TTTTGAATTA CCATTTTTT ATAAAAAAA 1952	
2752	(2) INFORMATION FOR SEQ ID NO: 32:	
2753	(i) SEQUENCE CHARACTERISTICS:	
2754	(A) LENGTH: 175 amino acids	
2755	(B) TYPE: amino acid	
2756	(D) TOPOLOGY: linear	
2758	(ii) MOLECULE TYPE: peptide	
2760	(vi) ORIGINAL SOURCE:	
2761	(A) ORGANISM: Mouse	
2763	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:	
2765	Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys Ala	
2766	5 10 15	
2767	Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln Asp	
2768	20 25 30	
2769	Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly Met	
2770	35 40 45	
2771	Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly Thr	
2772	50 55 60	
2773	Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys Gly	
2774	65 70 75 80	
2775	Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu Leu	
2776	85 90 95	
2777	Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His Glu	
2778	100 105 110	
2779	Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His Arg	
2780	115 120 125	
2781	Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala Cys	
2782	130 135 140	
2783	Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser Ala	
2784	145 150 155 160	

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001
TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRF3\10152001\I039177D.raw

2785 Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro
E--> 2786

165

170

2909 (2) INFORMATION FOR SEQ ID NO: 35:

2910 (i) SEQUENCE CHARACTERISTICS:

2911 (A) LENGTH: 536 amino acids

2912 (B) TYPE: amino acid

2913 (D) TOPOLOGY: linear

2915 (ii) MOLECULE TYPE: peptide

2917 (vi) ORIGINAL SOURCE:

2918 (A) ORGANISM: MOUSE

2920 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

2923 Met Thr Ala Pro Trp Ala Ala Leu Ala Leu Leu Trp Gly Ser Leu Cys
2924 5 10 15
2926 Ala Gly Ser Gly Arg Gly Glu Ala Glu Thr Arg Glu Cys Ile Tyr Tyr
2927 20 25 30
2928 Asn Ala Asn Trp Glu Leu Glu Arg Thr Asn Gln Ser Gly Leu Glu Arg
2929 35 40 45
2930 Cys Glu Gly Glu Gln Asp Lys Arg Leu His Cys Tyr Ala Ser Trp Arg
2931 50 55 60
2932 Asn Ser Ser Gly Thr Ile Glu Leu Val Lys Lys Gly Cys Trp Leu Asp
2933 65 70 75 80
2934 Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Val Ala Thr Glu Glu Asn
2935 85 90 95
2936 Pro Gln Val Tyr Phe Cys Cys Cys Glu Gly Asn Phe Cys Asn Glu Arg
2937 100 105 110
2938 Phe Thr His Leu Pro Glu Pro Gly Gly Pro Glu Val Thr Tyr Glu Pro
2939 115 120 125
2940 Pro Pro Thr Ala Pro Thr Leu Leu Thr Val Leu Ala Tyr Ser Leu Leu
2941 130 135 140
2942 Pro Ile Gly Gly Leu Ser Leu Ile Val Leu Leu Ala Phe Trp Met Tyr
2943 145 150 155 160
2944 Arg His Arg Lys Pro Pro Tyr Gly His Val Asp Ile His Glu Val Arg
2945 165 170 175
2946 Gln Cys Gln Arg Trp Ala Gly Arg Arg Asp Gly Cys Ala Asp Ser Phe
2947 180 185 190
2948 Lys Pro Leu Pro Phe Gln Asp Pro Gly Pro Pro Pro Ser Pro Leu
2949 195 200 205
2950 Val Gly Leu Lys Pro Leu Gln Leu Leu Glu Ile Lys Ala Arg Gly Arg
2951 210 215 220
2952 Phe Gly Cys Val Trp Lys Ala Gln Leu Met Asn Asp Phe Val Ala Val
2953 225 230 235 240
2954 Lys Ile Phe Pro Leu Gln Asp Lys Gln Ser Trp Gln Ser Glu Arg Glu
2955 245 250 255
2956 Ile Phe Ser Thr Pro Gly Met Lys His Glu Asn Leu Leu Gln Phe Ile
2957 260 265 270
2958 Ala Ala Glu Lys Arg Gly Ser Asn Leu Glu Val Glu Leu Trp Leu Ile
2959 275 280 285
2960 Thr Ala Phe His Asp Lys Gly Ser Leu Thr Asp Tyr Leu Lys Gly Asn
2961 290 295 300

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001
TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRF3\10152001\I039177D.raw

2962 Ile Ile Thr Trp Asn Glu Leu Cys His Val Ala Glu Thr Met Ser Arg
2963 305 310 315 320
2964 Gly Leu Ser Tyr Leu His Glu Asp Val Pro Trp Cys Arg Gly Glu Gly
2965 325 330 335
2966 His Lys Pro Ser Ile Ala His Arg Asp Phe Lys Ser Lys Asn Val Leu
2967 340 345 350
2968 Leu Lys Ser Asp Leu Thr Ala Val Leu Ala Asp Phe Gly Leu Ala Val
2969 355 360 365
2970 Arg Phe Glu Pro Gly Lys Pro Pro Gly Asp Thr His Gly Gln Val Gly
2971 370 375 380
2972 Thr Arg Arg Tyr Met Ala Pro Glu Val Leu Glu Gly Ala Ile Asn Phe
2973 385 390 395 400
2974 Gln Arg Asp Ala Phe Leu Arg Ile Asp Met Tyr Ala Met Gly Leu Val
2975 405 410 415
2976 Leu Trp Glu Leu Val Ser Arg Cys Lys Ala Ala Asp Gly Pro Val Asp
2977 420 425 430
2978 Glu Tyr Met Leu Pro Phe Glu Glu Glu Ile Gly Gln His Pro Ser Leu
2979 435 440 445
2980 Glu Glu Leu Gln Glu Val Val His Lys Lys Met Arg Pro Thr Ile
2981 450 455 460
2982 Lys Asp His Trp Leu Lys His Pro Gly Leu Ala Gln Leu Cys Val Thr
2983 465 470 475 480
2984 Ile Glu Glu Cys Trp Asp His Asp Ala Glu Ala Arg Leu Ser Ala Gly
2985 485 490 495
2986 Cys Val Glu Glu Arg Val Ser Leu Ile Arg Arg Ser Val Asn Gly Thr
2987 500 505 510
2988 Thr Ser Asp Cys Leu Val Ser Leu Val Thr Ser Val Thr Asn Val Asp
E--> 2989 515 520 525
2990 Leu Leu Pro Lys Glu Ser Ser Ile
E--> 2991 530 535
3081 (2) INFORMATION FOR SEQ ID NO: 37:
3082 (i) SEQUENCE CHARACTERISTICS:
3083 (A) LENGTH: 97 amino acids
3084 (B) TYPE: amino acid
3085 (D) TOPOLOGY: linear
3087 (ii) MOLECULE TYPE: peptide
3089 (vi) ORIGINAL SOURCE:
3090 (A) ORGANISM: C. elegans
3092 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:
3095 Cys His Cys Ser Arg Glu Val Gly Cys Asn Ala Arg Thr Thr Gly Trp
E--> 3096 5 10 15
3097 Val Pro Gly Ile Glu Phe Leu Asn Glu Thr Asp Arg Ser Phe Tyr Glu
E--> 3098 20 25 30
3099 Asn Thr Cys Tyr Thr Asp Gly Ser Cys Tyr Gln Ser Ala Arg Pro Ser
E--> 3100 35 40 45
3101 Pro Glu Ile Ser His Phe Gly Cys Met Asp Glu Lys Ser Val Thr Asp
E--> 3102 50 55 60
3103 Glu Thr Glu Phe His Asp Thr Ala Ala Lys Val Cys Thr Asn Asn Thr
E--> 3104 65 70 75 80

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001
TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRF3\10152001\I039177D.raw

3105 Lys Asp Pro His Ala Thr Val Trp Ile Cys Cys Asp Lys Gly Asn Phe
E--> 3106 85 90 95
3107 Cys
3111 (2) INFORMATION FOR SEQ ID NO: 38:
3112 (i) SEQUENCE CHARACTERISTICS:
3113 (A) LENGTH: 6 amino acids
3114 (B) TYPE: amino acid
3115 (D) TOPOLOGY: linear
3117 (ii) MOLECULE TYPE: peptide
3119 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:
3121 Asp Leu Lys Pro Glu Asn
E--> 3122 5
3128 (2) INFORMATION FOR SEQ ID NO: 39:
3129 (i) SEQUENCE CHARACTERISTICS:
3130 (A) LENGTH: 6 amino acids
3131 (B) TYPE: amino acid
3132 (D) TOPOLOGY: linear
3134 (ii) MOLECULE TYPE: peptide
3136 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:
3138 Asp Leu Ala Ala Arg Asn
E--> 3139 5
3142 (2) INFORMATION FOR SEQ ID NO: 40:
3143 (i) SEQUENCE CHARACTERISTICS:
3144 (A) LENGTH: 6 amino acids
3145 (B) TYPE: amino acid
3146 (D) TOPOLOGY: linear
3148 (ii) MOLECULE TYPE: peptide
3150 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:
3152 Asp Ile Lys Ser Lys Asn
E--> 3153 5
3156 (2) INFORMATION FOR SEQ ID NO: 41:
3157 (i) SEQUENCE CHARACTERISTICS:
3158 (A) LENGTH: 6 amino acids
3159 (B) TYPE: amino acid
3160 (D) TOPOLOGY: linear
3162 (ii) MOLECULE TYPE: peptide
3164 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:
3166 Asp Phe Lys Ser Lys Asn
E--> 3167 5
3170 (2) INFORMATION FOR SEQ ID NO: 42:
3171 (i) SEQUENCE CHARACTERISTICS:
3172 (A) LENGTH: 6 amino acids
3173 (B) TYPE: amino acid
3174 (D) TOPOLOGY: linear
3176 (ii) MOLECULE TYPE: peptide
3178 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:
3180 Asp Leu Lys Ser Ser Asn
E--> 3181 5
3184 (2) INFORMATION FOR SEQ ID NO: 43:

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001
TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRF3\10152001\I039177D.raw

3185 (i) SEQUENCE CHARACTERISTICS:
3186 (A) LENGTH: 6 amino acids
3187 (B) TYPE: amino acid
3188 (D) TOPOLOGY: linear
3190 (ii) MOLECULE TYPE: peptide
3192 (ix) FEATURE:
3193 (D) OTHER INFORMATION: First Xaa is Thr or Ser;
3194 fourth Xaa is Tyr or Phe; Each other Xaa
3195 may be any amino acid
3197 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

W--> 3199 Gly Xaa Xaa Xaa Xaa Xaa

E--> 3200 5

3203 (2) INFORMATION FOR SEQ ID NO: 44:
3204 (i) SEQUENCE CHARACTERISTICS:
3205 (A) LENGTH: 6 amino acids
3206 (B) TYPE: amino acid
3207 (D) TOPOLOGY: linear
3209 (ii) MOLECULE TYPE: peptide
3211 (ix) FEATURE:
3212 (D) OTHER INFORMATION: Fisrt Xaa is any amino acid;
3213 second Xaa is Ile or Val;
3214 third Xaa is Lys or Arg;
3215 fourth Xaa is Thr or Met.

3217 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

W--> 3219 Xaa Pro Xaa Xaa Trp Xaa

E--> 3220 5

3223 (2) INFORMATION FOR SEQ ID NO: 45:
3224 (i) SEQUENCE CHARACTERISTICS:
3225 (A) LENGTH: 6 amino acids
3226 (B) TYPE: amino acid
3227 (D) TOPOLOGY: linear
3229 (ii) MOLECULE TYPE: peptide
3231 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

3233 Gly Thr Arg Arg Tyr Met

E--> 3234 5

3236 (2) INFORMATION FOR SEQ ID NO: 46:
3237 (i) SEQUENCE CHARACTERISTICS:
3238 (A) LENGTH: 6 amino acids
3239 (B) TYPE: amino acid
3240 (D) TOPOLOGY: linear
3242 (ii) MOLECULE TYPE: peptide
3244 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

3246 Gly Thr Ala Arg Tyr Met

E--> 3247 5

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001
TIME: 13:47:05

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRF3\10152001\I039177D.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:85 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:98 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:1
M:254 Repeated in SeqNo=1
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:207 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:209 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:213 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:217 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:221 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:225 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:229 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:233 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:236 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:238 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:340 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:353 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:3
M:254 Repeated in SeqNo=3
L:357 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:442 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:444 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:448 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:452 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:456 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:460 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:464 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:468 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:472 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:476 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:480 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:484 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:488 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:542 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:632 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:645 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:5
M:254 Repeated in SeqNo=5
L:721 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:723 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:727 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:731 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:735 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:739 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:743 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:747 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:751 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:755 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:759 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5

VERIFICATION SUMMARY DATE: 10/15/2001
PATENT APPLICATION: US/09/039,177D TIME: 13:47:05

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRF3\10152001\I039177D.raw

L:763 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:767 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:771 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:775 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:779 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:783 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:787 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:791 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:794 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:796 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:940 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1080 M:254 E: No. of Bases conflict, Input:0 Counted:1585 SEQ:7
M:254 Repeated in SeqNo=7
L:1210 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1223 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:9
M:254 Repeated in SeqNo=9
L:1227 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1389 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1479 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1492 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:11
M:254 Repeated in SeqNo=11
L:1727 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1740 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:13
M:254 Repeated in SeqNo=13
L:1750 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1992 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2133 M:254 E: No. of Bases conflict, Input:0 Counted:1584 SEQ:15
M:254 Repeated in SeqNo=15
L:2253 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2266 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:17
M:254 Repeated in SeqNo=17
L:2503 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2521 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2539 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2557 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2575 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2593 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2611 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2630 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:2786 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:32
L:2989 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
M:332 Repeated in SeqNo=35
L:3096 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:37
M:332 Repeated in SeqNo=37
L:3122 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:38
L:3139 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:39
L:3153 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:40
L:3167 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:41
L:3181 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:42

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/039,177D

DATE: 10/15/2001
TIME: 13:47:05

Input Set : A:\Lud-5539 sequence listing.txt
Output Set: N:\CRF3\10152001\I039177D.raw

L:3199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:3200 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:43
L:3219 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:3220 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:44
L:3234 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:45
L:3247 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:46

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- 7. Other: _____

Applicant Must Provide:

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support (SIRA)

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

RECEIVED

NOV 13 2001

Raw Sequence Listing Error Summary
TECH CENTER 1600/2900

ERROR DETECTED	SUGGESTED CORRECTION ..	SERIAL NUMBER: 09/0391771D
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPIIA" HEADERS, WHICH WERE INSERTED BY P		
1 <input checked="" type="checkbox"/> Wrapped Nucleic <input checked="" type="checkbox"/> Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino <input type="checkbox"/> Numbering	The numbering under each 3 rd amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 <input type="checkbox"/> "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences <input type="checkbox"/> (OLD RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (ii) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences <input type="checkbox"/> (NEW RULES)	Sequence(s) ____ missing. If Intentional, please insert the following lines for each skipped sequence <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's <input type="checkbox"/> (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents	
10 <input type="checkbox"/> Invalid <213> <input type="checkbox"/> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 <input type="checkbox"/> "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	"n" can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

AMC/MH - Biotechnology Systems Branch - 08/21/2001

Error Summary Sheet
See Error Summary Supplement